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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	June 23, 2003, 12:51:58; Search time 8181 Seconds (Without alignments) 11586.339 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-817-198B-1 3257 1 tgcccgctgcccgccgcagaaaaaaaaaaaaaaa
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 1: gb_ba:* 2: gb_htg:* 3: ah in:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ď			SUMMARIES	
Result No.	Score	Query Match	Ä	DB	В	Description
7	2696.6 1192.8	82.8 36.6	190517 7924	9	CNS01DX4 AX347040	AL139022 Human chr AX347040 Sequence
	1192.8		7924		AX348456	
ה ה ביה	1160.8		7924		AX347041 AX348457	AX347041 Sequence AX348457 Sequence
	1000.2		1054	9	AX399903	AX399903 Sequence
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	577.6	17.	945			M83679 Sprague-Daw
c 11	477.4	1.4	4 81 4 63			AX334820 Sequence
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n 13	416.4	12.	257226	250	BC013790 AC124556	BC013790 Mus muscu
	307	6	313			AX341683 Sequence
16 17	234.2		2048			BC002977 Homo sapi AK025165 Homo sapi
18	230.6	7	1980			S53268 Homo sapien
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51	227.4	7	638		\$53270	S53270 MEL-RAS-rel
53 53 53	224.2		1337		BC019990 CFRAB8	BC019990 Mus muscu X56385 Canine rab8
24	218.2	9	765		DYGORA2	M38391 Discopyge o
25 26	217.8	ف ف	624 1128		AX236078 BC020654	AX236078 Sequence BC020654 Homo sapt
27	217.8	6	1161		AX236076	AX236076 Sequence
7 58 7 7 8	217.8	6	1265		AB038995 AX285074	AB038995 Homo sapi AX285074 Sequence
30	217.8	٠٠٠	2497		AX285080	AX285080 Sequence
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30	198.0	ف د	110000		AC048347_0	ACU4834/ Homo sapi Continuation /2 of
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ACCESSION VERSION		39022	4 GI:14	41489	954	
KEYWORDS		HTG. human.				
ORGANISM		Homo sapiens Eukaryota; M	ens ; Metazoa;) a ;	ordata;	Craniata; Vertebrata; Euteleostomi;
REFERENCE		(bases	to 1	9051	דווומ רפט'י	attiitit, nomtiitaas, nomo.
AUTHORS		Heilig, R.,	Ъ	J. J.	Vico, V.,	Dasilva, C., Robert, C., Wincker, P.,
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/note="matching EMBL:L00635 RHdb:RH53755 Ghartified using the e-PCR software (G. Schuler)* A7222. 47411 A7222. 47411 A7222. 47411 STS HRdb:RH48340 GhSTS:STS31599 STS L128437 Anote="matching EMBL:GO7550 RHdb:RH34434 GhSTS:STS375 Anote="matching EMBL:GO7550 RHdb:RH34849 GhSTS:STS375 Anote="matching EMBL:GO7550 RHdb:RH34849 RHdb:RH34849 Anote="matching EMBL:AA160869 RHdb:RH348136 Anote="matching EMBL:AA160869 RHdb:RH348149 Anote="matching EMBL:M56308 RHdb:RH348149 Anote="matching EMBL:W56308 RHdb:RH348149 Anote="matching EMBL:W56308 RHdb:RH34096 Anote="matching EMBL:S39018 RHdb:RH361814090 Anote="matching EMBL:R10900 RHdb:RH37191 Anote="matching EMBL:R10900 RHdb:RH37191 Anote="matching EMBL:R10900 RHdb:RH37191 Anote="matching EMBL:R10900 RHdb:RH37191 Anote="matching EMBL:G27797	Dase Courr 52747 a 43175 c 42572 g 52023 t Couler)
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J. JOUGNAL Upublished Upu	Percentage of bases with a quality value >= 40: 99 %. FEATURES Source / Cocation/Qualifiers SOURCE Accountion Accountic Accountic Accoun

1973 GCTTGGTGCTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGCCCTCTACCTCCTG 20	2033 159179	2093 159239	2153 159299	2213 TCCCAAGGTGGGCGAGGCCTAGGAAGAGGTCATTCTTAAGCCACATAGCTGCACTG 2272	2273 CGTGGCTGCAGCCAAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAT 2332 	2333	2393 GGGAAAGAACCATCAAACCTTCCTCGTGACTTACCAAACCAGGAAAACAGCAGGAGGG 2452 	2453 GIGGCTCAGGACTIAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAAGGAGGAGGA 2512 	2513 159659	2573 159719	2633 ACACTGGGGCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCT	2693 GAGAAGTTATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAG 2752 	2753	2813 ATTGTACTGTACCCTAGGGGTTCTGGAAGGAAAACATGGAATCAGGATCTAGACT 2872	2873 GATAGGCCCTATCCACAAGGCCATGACTGGAAAAGGTATGGGAACGAAGGAATTG 2932	2933 GGATTITAGGGTGCAGCTACCCTAAACTITIGGTGGCCTGGGGCAIGTCTTGAG 2992	2993 GCCCAGACTGTTAAGCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCT 3052	3053 GTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCC 3112
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481 TTAGGGATAGTACTATAGTAGAGGGAATGTAGTAATACTAGGTTTTTTAGGTTT 540 1816 CATCTTCCATTTCTTAGGTAAGAAGAGCATTTCCTCAGACTCCAGGCGGAGGACTGAC 1875	1996 FITAAGACAAAGCCCTATCTTCCTACACCCCGAACCAGGGGCCCCACC 2055 1916	O CIGORANGOSARANGOSARANGOSARIONANGARANGOCOLARIONANGOCOLA 2007 ON CONTROLARIONANGOCOLARIONA
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OY 2896 ATGACTGGGAAAAGGTATGGGAATTGGGATTTAAGGGTGCAGCTACGCT 2955	RESULT 3 AX348456 LOCUS	tch 36.6%; Score 1192.8; al Similarity 75.8%; Pred. No. 2.2 1476; Conservative 0; Mismatches 276 GGTGCTTCTCCTCTCCCCCACCCCTGTC

TAACCTACGAAAATAAAAAAAAAAAAAAAAAAAAAAAAA	7502 ACATTTAAAAATAAAAAACTAACTCCTATATATCAAATTAAAAACAAAAAA	2058 ACTGTGGCTACAGGTGGAAGAGGACTCCTTCCTCCACAGTGCTATGTTCAGGAAGT 2117
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	1741 GTTGCTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	VERSION AX347041.1 GI:18494929 KEEYWORDS SOURCE Synthetic construct. ORGANISM artificial sequences. REFERENCE 1 AUTHORS Olek,A., Piepenbrock,C. and Berlin,K. TITLE Diagnosis of diseases associated with the immune system JOURNAL Patent: WO 0200928-A 2112 03-JAN-2002; EATURES Location/Qualifiers JOGALON/QUALIFIERS Location/Qualifiers FEATURES 1. 7924 /Organism="synthetic construct" //note="chemically treated genomic DNA (Homo sapiens)" BASE COUNT 1973 a 83 c 1827 g 4041 t ORIGIN QUETY MATCh BASE Local Similarity 74.1%; Pred. No. 4.1e-288; MATCHES 1468; CONSERVATIVE 0; Mismatches 512; Indels 0; Gaps 0; MATCHES 1468; CONSERVATIVE CCCCACCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCACTGCCCTCCCCCACTGCCCTCCCCCACTGCCCCCCCC

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                                      Query Match
Best Local Similarity 74.1%;
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whethod and nucletc acids for pharmacogenomic methylation analysis
Patent: WO 0202806-A 152 10-JAN-2002;
Epigenomics AG (DE)
                                                                                                                                                                                                                                                  TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATTTGGGCAGTGGCTC
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AX348457
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TITLE
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C 6903 A 2357 A 6843	T 2417 T 6783	T 2477 T 6723	A 2537 6663	A 2597 6603	ia 2657 	C 2717 C 6483	C 2777 C 6423	T 2837 6363	AT 2897 - AT 6303	2A 2957 2A 6243	3C 3017 	AG 3077 AA 6123	rg 3137 ra 6063	TA 3197 TA 6003	AA 3257 - AA 5943
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PAT 06-JUN-2002

linear

DNA

AX399903 1054 bp Sequence 74 from Patent WO0218424. AX399903

DEFINITION RESULT 6 AX399903 LOCUS

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                                                                                                                                                                              Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J., Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T. Nucleic acids and polypeptides
Patent: WO 0218424-A 74 07-MAR-2002;
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                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. 1054
/organism="Homo sapiens"
//db_xref="taxon:9606"
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Best Local Similarity 99.6
Matches 1002; Conservative
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FKMKTIDVDGIKVRIQIMDTAGQERYQTITKQYYRRAQGIFLYYDISSERSYQHIMKW
VSDVDEXAPECVQKILIGNRADEBQKRQVGREQGQDLAKEYGMDFYETSACIMLNIKE
SFTRLFELVLQAHKRIDGETRARANEIALAELEEDEGKPEGPANSSKTCWC"
84.7 87.8 9 691 t
            Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,R., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone_lib="NC1_CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                                   found
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                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"Unknown (protein for MGC:38375)"
/protein_id-"AAH27769.1"
/db_xref-"GI:20380722"
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Pred. No. 2.1e-198;
                                                                                                                                                                                                                                                                                                                                   /clone="MGC:38375 IMAGE:5345297"
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208. .846
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1, 3139
Corganism="Mus musculus"
Ab xref="taxon:10090"
/map="FVB/N"
 http://www.nisc.nih.gov/
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llarity 67.4%;
Conservative
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                                                                                                                                             AGGCAAGAGCGGATCCGAAGGGCGGCTCCTAGAACCAGGGTTAGAGCAAGAGCAGAGGG 1848
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                                                                                                                      GGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGAGCAAGGGAGAGCT 1753
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                                   ---TCTCCTCACCTGGATTCACAATTTAAAGATGGGGATCGAGGTCTGAGGACAC-CA
CGATGGGGTGGCAGGGAT - - TAAGTCACCTCTGTTCTCTACCTCCCATGCCTC - - - - - -
                        CAATTICICICCACCIGGCICCCAAATTTAAAGAIGIGGACCAAGGCCIGIGGGIACICC
                                                                       AGGGCAAGGAGCCCTGGGGTCAGTGACACTGTCAGGCCAACCATGCACTCCACAAAG
                                                                                    GGCCAGGGACAGCAGTTTGCACAGCAGAGGAATGTAGCAACAGGGGCTCCTAGGC
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ROD 27-APR-1993

Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds. M83679.1 GI:206536

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/protein_id="AaA41995.1"

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/Lanslation="AkkQyDVI"

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FKWKTIEVDGIKVRIQIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKW

VSDVDEXAPEGVQKILIGNKADEEORRQVGREQGQOLAKEYGMDFYETSACTRINIKE

STRALFLUQAHRKELDGORRQVGREQGQOLAKEYGMDFYETSACTRINIKE

STRALFLUQAHRKELDGORRQVGREGGOLAKEYGMDFYETSACTRINIKE

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                                                                Craniata; Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
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                                                                                                                                                  protein
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LAWW GTP-binding protein.
Rattus norvegicus (strain Sprague-Dawley) (library:
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                              1 (bases 1 to 945)
Elferink,L.A., Anzai,K. and Scheller,R.H.
rabl5, a novel low molecular weight GTP-binding |
specifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
1313420
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Pred. No. 1e-137;
0; Mismatches 79;

    945
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                   /tissue_lib="LAMBDA ZAPII"
1. 945
/gene="RAB15"
                                                                                                                                                                                                                                                                           /strain="Sprague-Dawley
/db_xref="taxon:10116"
/tissue_type="brain"
                                                                                                                                                                                                                            Location/Qualifiers
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/gene="RAB15"
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11 Similarity 88.78;
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QY 3002 GTTAAGCAGGCTCTGCTGGCCTGTTTACTCGTCACCTCTGCACCTGCTGTCTTGAGA 3061 Db 421 GTTAACCAGGCTCTGCTGTTTACTCGTCACCACCTNTGCACCTGTTTACTTGAGA 480 QY 3062 C 3062 Db 481 C 481	RESULT 11 AX334820/c LOCUS DEFINITION Sequence 5329 from Patent W00194629. ACCESSION AX334820 VERSION AX334820.1 GI:18125539	NETHERENCE TOURNELS Caniata; Vertebrata; Eutelecitomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecitomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., TITLE Cancer gene determination and therapeutic screening using signature gene sets JOURNAL Patent: WO 0194629-A 5329 13-DEC-2001; REATURES 1 463 Source 1 463	9606") g 1 ore 438. ed. No. Mismatc	2790 CCCCTCAGGAAAGGACTAIATTTGIACTGIACCCTAGGGGTTCTGGAAGAAAAC	Db 393 ATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAG 334 Qy 2910 GTATGGGAGCAGAAAGTGGGATTTTAGGGTGCAGCTACCCTCACCTTAACTTTT 2969		OY 3090 CTCCTGAGCCTCCACTATCTCCCTGTGAACTTCGTGTACTTCTGGGTCC 3149	3210 TATTCAAACCACCAAAAAAAAAAAAAAAAA 3243
Qy 501 TGCACCAACGTCAACATTAAAGAGTCATTCACGCGTCTGACAGAGCTGGTGCTGCAGGCC 560	Qy 621 CTGGAGGAGGAGGCAAACCCGAGGACTCTTCGAAAACCTGCTGCTGC 680	AX396088 AX396088 AX396088 AX396088 AX396088 AX396088 AX396088 AX396088 AX396088 ACCESSION AX396088 AX396088 AX396088 AX396088 ACCESSION AX396088 AX39608 AX	Composition of the concer Patent: W CORIXA CO	### ACCOUNT 111 a 113 c 130 g 125 t 2 others ORIGIN Query Match	2582 GTTGCTTCCTTGAAGATGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGG	61 CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTA 2702 TATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTCCTGAAGATCAGGCAG	Qy 2762 GGTGCCATTGTCTTCTCTCTCCTGGGAAAGGAGCTATATTGTCTT 2821 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 2882 TATCCACAAGGCCATGACTGGGAAAAGGTATGGGAGTTTTAG 2941 Db 1

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COMMENT
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Standy D. Marle, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alabrooks, S., Amin, A., Anquiano, D., Alder, J., Alabrooks, S., Amin, A., Anquiano, D., Anyalabechil V., Asyaqia, A., Asyaqia, N., Baca, E., Baden, H., Baldwih, D., Bandaranalka, D., Barber, M., Baca, E., Baden, H., Baldwih, D., Bandaranalka, D., Barber, M., Barnstead, M., Benahmed, F., Blydan, C., Carter, K., Cavazos, I., Ceast, H., Center, A., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, G., Dezano, C., Bederich, D., Dadyado, O., Denson, S., Deramo, C., Digg, Y., Dinh, H., Divya, K., Dadyado, O., Denson, S., Deramo, C., Boyas, C.A., Falls, T., Fan, G., Franch, E., Scotto, M., Eagen, C., Evans, C.A., Falls, T., Fan, G., Franche, F., Badhish, A., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Grady, M., Gebrea, M., Garcia, A., Garrer, M., Gebregocrajs, E., Geer, K., Gill, R., Crady, M., Hamilton, K., Hamilton, K., Harliton, K., Harliton, K., Marliton, K., Marliton, K., Marlinoud, M., Malloson, R., Johnson, B., Morshea, J., Liu, J., Liu, M., Liu, Y., Landar, F., Marlin, R., Martin, M., Man, M.,
162495 bp DNA linear HTG 24-AUG-2002
Rattus norvegicus clone CH230-16122, *** SEQUENCING IN PROGRESS
***, 70 unordered pieces.
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Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 11551 bases at least Q40
Consensus quality: 123470 bases at least Q30
Consensus quality: 127758 bases at least Q30
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Db 125410 CCCTCCCCCAGTCCCCTCAGGAGGCCCGTGGAGGCAGGGAGTCTGGGCTTTG 125354	QY 821 GCCTGGCCCTGAGAGCGGCTCTGCTGTCATCT-CAAGCAGCCCCTGTCCCAGCCCGTCC 879	QY 880 ACCTGGAGIGTTTTTTCAGCTGTTTCCCCAGCCACAGGCCTGGTACGACCCCCACG 939 125235 ATCTGGAGIGGTAACCTTTCACCTGTTTCCCAGCCGCAGGCCTGCTGTACACCC 125180	QY 94.0 AIGTGCCGCAAGCACTGTCTCACCACCCCCCCCCCCACCAGCACAACAGCCCGGGCTGGAGT 999 125179 AGAATGTGCTTCGACCATCTCACCAACCCCAGGCTCTGGGACAAGGTCAAGGTTGAGGTGAAGTTGAGCTTCAACCCAACCCCAGGCTCTGGGACAAGGTCAAGGTTGAAGGTGAACTGACAACCCAAGCTCTGGGACAACGGTCAAGGTGAAGGTGAAGGTTGAAGAGTTGAACAACCCAAGCTCTGGGAAAAAAAA	QY 1000 CCAGGCCACTTTCAGCTGCTCTTTCTCCGTGCATGGTGTCTCTTCTCTGCTTTTCTCT 1059	QY 1060 CTTCCCCACTTCTCTGACCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCT 1119	QY 1120 CAAACCCGTGCCCCGTGTGTCCTGCTGTGTGCAGCTCGCTTTCCTTCC	QY 1180 TATCCAAGGGATGGACCCAGGCTCGTGGGAGGTTCCACCTTGGATCCAGGAAGAACC 1239	QY 1240 CTCCACCTGCCTCGTGGGCCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCACC 1299 Db 124901.GCTCACCCTG-CTCTGGGCTGGCTGAAGGCTA-AGGGTGCTTCTTCCTCTCCCCTC 124846	QY 1300 CCCACTGTCCCTCATGTGCCATGGCCTGCCTCCCCAGTGACCTGCGGAAAGTGGAGCATC 1359	QY 1360 GAGGTAGGAGGGAAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACC 1419	QY 1420 CATTCCCGACCAGAGCTTGCCCTTGCTTGGCTGCCTCTCTGGGGAACTGA 1479 124728 TTGCCTTCTGCTGGAGTTTTGGCTTGCTGGCTGCCTACTGCCTGC		1540 ACCTCCATTCTCTACCTCCCATGCAGCATGAACACTTTCTCTCCACCTGGCTCCCAAA	11	1000 IGATALISICANGCERNOCARIOCARIOCARIOCARIOCARIOCARIOCARIOCARI	1/20 CICCIACIAIN CONSTITUENCE ANACISCOCCACOCACACACACACACACACACACACACACACACA	OY 1//9 AGAGGGGAATGTAGCAGGGGGGGGGGGGGGGGGGGGGGG
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FRMKTIDVDGIKVRIQIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKW
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S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 5 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAGCAAGGGCAGCAGCAGCGAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCACTCCTCGCATATCTCCACCATCGGTGTTGACTTTAAGATGAAGACTATCGATGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 TCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTGGTCTATGACATTAGCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 AGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGATGAGTACGCACAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 TGATCGGGGACTCCGGGGTGGGCAAGACCTGCCTGTGTGCCGCTTCACCGACAACGAGT
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Unknown (protein for MGC:6897)"
/protein_id="AAH13790.1"
/db_xref="GI:15489394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                     Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcla, A.M., Lu, X., Hulyl
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N-3"
/clone="MGC:6897 IMAGE:2655151"
/tissue_type="Mammary tumor. MMTV
old mouse. Taken by biopsy."
/clone_lib="MCI_CGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 416.4; DB 1
Pred. No. 5.1e-96;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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Best Local Similarity 91.5%;
Matches 441; Conservative
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                                    124091 AAGGACA---CCTCCACAGAGTTCTATGCTCAGGAAGTTTCTTTAACCC--TGTGGCCC 124037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcU13790 2560 bp mRNA linear ROD 07-AUG-2002
Mus musculus, clone MGC:6897 IMAGE:2655151, mRNA, complete cds.
BC013790
                                                                                                                                                                                                                                                                                                                                                                                                                                             2249
                                                                                     1959 CCCTGGGTAGAAACGCTTGGTGCTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTG 2018
                                                                                                                                                                                                                             CCCTCTACCTCCTGATAGGCTTGAGGGTTTGCCAACCACACTGTGGCTACAGGTGGAGGG 2078
                                                                                                                                                                                                                                                                                                AAGAGGACTCCTTCCTCCAGAGTGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCC 2138
                                                                                                                                                                                                                                                                                                                                                                      AAGAGTAGCTCGTAGGAGGCCCTT-----TAAAGACGGAACAAGTAATTTACCAGT 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2250 TAAGCCACACATTAGCTGCACTGCGTGGCTGCAAAACAAAGAACTGGGTGTTGAGT 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2310 ATTCATCAACTAAGAACCA------AAATCCAGGGCACTCATATGTGAAGGATAA 2358
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                    AGAGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGCCTAGGCCTTCAGCAACCAAGGTTC
                                                                                                          2190 TCTACTGGGGTTCCTGCCCACGTCCCAAGGTGGGCGAGGGCCTAGGAAGAGGGTCATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 2560)
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TITLE
JOURNAL
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BC013790
LOCUS
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643 CCGAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCC 702
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                   unknown length
of 10415 bp in length
unknown length
of 29150 bp in length
                                                                                        unknown length
of 17825 bp in length
unknown length
                                                                                                                                                                     unknown length
of 46886 bp in length
                                                                                                                                                 of 18231 bp in length
                                                                                                                                                                                                                        74933 bp in length
                                                                                                                                                                                                                                                            contig of 1346 bp in length
gap of unknown length
contig of 1777 bp in length
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                                                                                                                                                                                                        unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.6%; Score 378.4; DB 2
Best Local Similarity 61.2%; Pred. No. 7.8e-86;
Matches 1205; Conservative 0; Mismatches 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16762. 57176
/note="assembly_name:Contig15"
57277. 86426
/note="assembly_name:Contig16"
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/note="assembly_name:Contig17"
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22783. 169668
"note="assembly_name:Contig19"
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/note="assembly_name:Contig20"
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note="assembly_name:Contig10"
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246248. 248024
//note="assembly_name:Contig7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus'
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                           : contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'chromosome="UNK"
'clone="RP23-246K11"
                                                                      contig
gap of
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                                                                                                                                                                     AC124556 257226 bp DNA linear HTG 23-JUN-2002
Mus musculus chromosome UNK clone RP23-246K11, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louls, MO 63108, USA 3 (bases 1 to 257226) McPherson, J D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jun 23, 2002 this sequence version replaced 91:21426694.
551 GAGAGCAGGGCAGCAGCTGGCTAAGGAGTACGGCATGGACTTCTACGAAACAAGTGCCT 610
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalla; Eutherla; Rodentia; Sciurognath1; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer FT; 0% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 249197 bases at least Q40
Consensus quality: 252159 bases at least Q30
Consensus quality: 252159 bases at least Q20
Insert size: 214000; agarose-fp
Insert size: 23826; sum-of-contigs
Quality coverage: 9.36 in Q20 bases; sum-of-contigs
Quality coverage: 7.92 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
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gap of unknown length
contig of 15017 bp in length
gap of unknown length
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contig of 9622 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project information --
                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 257226)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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	135269 CTGAGGGCCCAGCAAACTCTTCAAAGACCTGCTGGTGCTGAGGGTTCTGAGTGGAGTCCC 135210	ò	CAGCACAGAGAGAAATGTAACAAACAACAGGACTOTTOTAAGAGAATGTAAAAAAATGTAACAAAAAAAAAA
Q.Y.	703 ACACGACACCCTTTCCCTCAGGAGCCCGTGGGCACCAGGGGAGCCGGGGCTTGCC 762	3 8	
λ̈́o	763 CTGCTGCTGTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGC 822	Å å	1835 AAGAAGAGCATTTCCTCAGACTCCCGGGGGGGAGGACTGAGCCTTCAGCAACCAAG 1894
g G	135156 C-ACCACCGTCCTTTCATTTGACAATCCTGTTGAAAACCAGTAGCTGCTACT-CCCCTGC 135099	l ò	GTTCTCCTGGGACCCAAAGTTTATGGGAAGAAGGGCAAAGACTTCATGGGAAGAGAAAG
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<u> </u>	941 TGTGCCGCAAGCACTGTCTCACCACCCGCACCACCACAACAACAGGCGGGGGTGGAGTC. 1000 11111 1 1 1 1 1 1 1 1	q	
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oy ep	1361 AGGTAGGAGAAACAGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCC	Qy Dp	2418 CCTGACTTACCAAACCAGGAAAACAGCAGGAGGGTGGCTCAGGACTTA 2467
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	1481 CTCAGAGGCAGCTCCAGAGAAGGAAACAAATGAGGGGTGGCAGGGATAAA 1534	ACCESSION VERSION KEYWORDS	AX341683.1 GI:18137665
oy D	1535 AAGTCACCTCCATTCTCTACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTC 1594	SOURCE ORGANISM	numan. NISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Enthoria: Drimatos: Catarrhin; uominidas; uomo
	CCAAATTTAAAGATGTGGACCAAGGCCTGTGGGTACTCCAGGGGCAAGGAGGCCTGGG	REFERENCE AUTHORS TITLE	1 Jiang, Y., Harlocker, S.L. and S Compositions and methods for
		JOURNAL	Cancer Patent: WO 0196388-A 1930 20-DEC-2001;
		FEATURES Sou	COKIAA CORPORATION (US) Location/Qualiflers rce 1313
	1715 ACTAGCTCCTATGTATCAGGTTAAGAGCAAGGGAGACGGCCAGGGACAGCAGTTGCA 1774	BASE COUNT	/organism="Homo sapiens" ./db_xref="taxon:9606" JUNT 68 a 85 c 85 g 73 t 2 others

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<pre>Query Match 9.4%; Score 307; DB 6; Length 313; Best Local Similarity 99.0%; Pred. No. 6.1e-68; Matches 308; Conservative 1; Mismatches 2; Indels 0; Gaps 0;</pre>	2824 ACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTA 2883	1 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATGGGCCCTA 60	Ĕ-	61 TCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGG 120	2944 TGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCCAGACTGT 3003	-⊢	04 TAAGCAGGCTCTGCTGGCTGTTTACTCGTCACCACCTCTGCACCTGTCTTGAGACT 3063		3064 CCATCCAGCCCCAGGCACCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTG 3123	-	24 AACTTCGTGTA 3134	
Query Match Best Local Simil Matches 308; C	2824 ACCC	1 ACC	2884 TCCA	61 TCCA	2944 TGCA	121 TGCA	3004 TAAG	181 TAAC	3064 CCAT	241 CCAT	3124 AACT	301 AACT
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Search completed: June 23, 2003, 15:56:06 Job time: 8188 secs

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S (HUMA-) HUMAN GENOME SCI INC Barash SC, Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ ID NO 37097; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to

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supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54921 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                   Sequence 3240 BP; 713 A; 882 C; 887 G; 758 T; 0 other;
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Pred. No. 0;
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Matches 2717; Conservative
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                                                                                                          1060 AGTTGTAAATCACTGGCTAATGAGAAAAGGGACAGCTAACTCTAGGATGAAGTGAC
                                                                                                                                                                           1000 TAGGCTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCAATC
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                                                             GTGGCTCAGGACTTAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGA
                                                                                                                                                         TAGGCTGGAGTTGCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATC
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                             GTGGCTCAGGACTTAGGGACAGGTATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGA
                                                                                                                                                                                                                        ATTIGIACTGIACCCIAGGGGITCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACT
                                                                                             <u> AGTTGTAAATCACTGGCTAATGAGAAAAGGAGACACCTAACTCTAGGATGAAGCTGTGAC</u>
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparationanis, nootropic; neuroprotective; categoratic; antiparkinsonian; nootropic; neuroprotective; categoratic; antiparkinsonian; nootropic; neuroprotective; categoratic; antipartin; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressant; antidabetic; hypotensive; dermatological; immunosuppressive; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic upper allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concernal hemenoglobinula, antiniflammatory disease; to enhance of contined in the propertion and as a contractorial contains.
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                  cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antlinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCCACCATCGGTGTTGACTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coagulation; to inhibit thrombosis; and as a contraceptive.
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; Pred. No. 0;
0; Mismatches
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                                                                                              thrombosis; contraceptive; ss.
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98.7%;
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02-APR-1999; 99US-0127636,
05-APR-1999; 99US-0127728,
30-MAR-2000; 2000US-0540763.
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Matches 1598; Conservative
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192 GRYGANGACCHANGACCHACANCACANCACANCTOGACACCTCCACCACCACACACACTCACCACCACCACCACACACACACACACACACACACACACA	1308 ACCTGCTCGTGGGCCAAAGGCTACAGGGGGCTTTTCCTTCC	RESULT 3 ABK40069 ID ABK40069 standard; DNA; 7924 BP. XX AC ABK40069; XX AC ABK40069; XX DT 21-MAY-2002 (first entry) XX DF Human chemically pretreated gene sequence #76 strand 1. XX XX XX XX KW Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; XX XX KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism. XX XX NOS Homo saplens. XX XX PN WO2002020806-A2. XX XX PD 10-JAN-2002.	PF 29-JUN-2001; 2001WO-EP07470. XX X
	182 GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 242 GATGAAGACCATAGAGGTAGACGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 242 GCAGGAGAACCATAGAGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 242 GCAGGAGAGAACCATCACAAAGCAGTACTATCTGCGGGGCCCAGGGGATATTTT 288 GCAGGAGAATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT 302 GGTCTATGACATTAGCAGCGACCTTATACCAGCACATCATGAAGTGGGTCAGTGACGT [S24 GTCATTCACGCGTCTGACAGAGCTGGTGCTGCAGGCCCATAGGAAGGA	### ### ##############################

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                                                                                                                                                                                                                                                                              each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPS (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 uncleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire. The vipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; antiinflammatory; cancer; action and alsease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzhelmer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 7924;
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Pred. No. 5e-279;
0; Mismatches 472; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2111; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7924 BP; 2087 A; 83 C; 2037 G; 3717 T; 0 other;
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75.8%;
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01-SEP-2000; 2000DE-1043826
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Matches 1476; Conservative
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                                                                                                                                                                                                                            Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                              AGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTAC
                     2956 CACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCCAGACTGTTAAGCAGGCTCT
                                                                                                                                                                                                                                                                               TGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTT
                                                                  GATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGC
                                                                                                                      2776 TCTTTCTCCTAGCCCCCTCAGGAAAGAAGACGACTATATTTGTACTGTACCCTAGGGGTT
                                                                                                                                                                         ATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCT
              2536 GAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTCCTTGAA
                                        GATGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGT
                                                                                                                                                                                                                                                                                                                                                                                              Human chemically pretreated gene sequence #76 strand 2.
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ABK40070 standard; DNA; 7924
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDHG (NW_000693), CYP11A (NW_000497), CYP3A3 (NW_000776 and NW_017460), DPYD (NW_000191), CYP11B1 (NW_0001979), CCLN (NW_001999), CCLN (NW_001999), CCLN (NW_001999), CCLN (NW_001990), CCLN (NW_001990), CCLN (NW_001990), NW_019901, NW_019902, NW_019908, NW_019909, NW_01990, N
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                                                                                                                                                                                                                                             New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                claim 1; SEQ ID No 152; 24pp; English
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2778 6422 2838 6362 2898 6302	Db 6242 CCCTAAACTITTAATAACTAAAACATTATAAACCAAACTATTAACCAAACTATTAACCAAACTATTAACCAAACTATTAACCAAACTATTAACCAAACTATTAACTAAACCTAAAACTATTAACTCGCACCACCACCAGGTCTTCAAACCTAAACTCCAAACCAGGTGAACTCCAAACCACCAGGTGAACTCCAACCCAGGTGAACTCCAACCCAAGAGTATAACAACCTCACCACCCAACCCAACCCCAAGAGTATAAACACCAACCCCAACCCCAAGAGTAACTAAC	ABL34139 standard; DNA; 7924 BP. XX XX AC ABL34139; XX	Homo sapiens. XX XX XX XX WC200200928-A2. XX WO200200928-A2. XX 03-JAN-2002. XX XX 02-JUL-2001; 2001WO-EP07537. XX XY XX XX
AGTGGCC 1757		CCTAGGAA 2237	
1688 ACCUTAGAAATCAATAACACTATCAAACCATACCATACACCTCCACAAAAAA		2178 TAATTTACCAGTTCTACTGGGGTTCCTGCCCACCGTCCCAAGGTGGGGGGGG	

associated The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukeamia, Albrimer's disease, AlbS, epllepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. German 2112; 32pp + Sequence Listing; 잁 a SEO ä Claim

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1877 1997 2057 1337 1457 1397 ö CATGGGAAGAGAGAAGGAAGAGCCTGGGTAGAAAAGGCTTGGTGCTGTTCTCTTTGGCCTT TICTCICCACCIGGCICCCAAAITIAAAGAIGIGGGCCAAGGCCIGIGGGIACICCAGGG TTCTCTCCCCCTAACTCCCCAAATTTAAAAATATAAAACCAAAACCTATAAATACTCCAAAA GCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGAGCAAGGGAGAGCTGGCC AGGGACAGCAGTTTGCACAGCAGAGGGGAATGTAGCAACAGCAGGGCCTCCTAGGCCCCCA TCTTCCATTTCTTAGGTAAGAGGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGCCT TCTTCCATTTCTTAAAAAAAAAAAAAATTTCCTCAAACTCCCAAAACGAAAAACTAAAACCT AGCCTTCAGCAACCAAGGTTCTCCTGGGACCCAAAGTTTATGGGAGAAGGCCAAAGACTT CATAAAAAAAAAAAAAAAAACCCTAAAATAAAAACGCTTAATACTATTCTCTTTAACCTT TAAGACAAAGCGCTCATCTTGCCCTCTACCTCCTGATAGGCTTGAGGGTTTGCCAACCAC TAAAACAAAACGCTCATCTTACCCTCTACCTCCTAATAAACTTAAAAATTTACCAACCAC **ACTGTGGCTACAGGTGGAGGGGAAGAGGACTCCTTCCTCCAGAGTGCTATGTTCAGGAAGT** TACTTCTTCCTCCTTCCCCCCCCCCCCCTCTATACCATAAACCTACCTCCCCAA GCCTGCCTCTTTGGGGAACTGAGCTCAGAGGCAGGTGCTTCAGAGAAAGGAAATGA GGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCATGCAGCATGAACACAAT GCAAGGAGACCCTGGGGTCAGTGACACTGTCAGGCCAACCATGCACTCCACAAAAGGGGA TGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACAGCAACCGGGGGAGTCCTCGAGC Gaps DB 24; Length 7924; ; 0 Score 1160.8; DB 24; Lengt Pred. No. 3e-271; 0; Mismatches 512; Indels Sequence 7924 BP; 1973 A; 83 C; 1827 G; 4041 T; 0 other; 35.6%; llarity 74.1%; Conservative Query Match Best Local Similarity Matches 1468; Conserv 1338 1398 7802 1458 7742 1518 7682 1578 7622 1638 7562. 1698 7502 1758 7442 1818 7382 1878 7322 1938 7262 1998 7142 ò g 9 07 9 9 9 9 9 9 g Q a 9 9 9 9 9 g à q 셤 à 셤 ö g 9 P ò

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                                  06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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20-OCT-2000;
20-OCT-2000;
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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08-SEP-2000;
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17-NOV-2000;
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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antilnflammatory; anti-HIV; antibacterial; antilnflammatory; cancer; limmune system disorder; rheumatold arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; inflammatory condition; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardlovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                                                                                                                                  cDNA encoding novel signal transduction pathway protein, Seq ID 88
                                                                                AAS27053 standard; cDNA; 2021 BP
                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180628.
2000US-0184664.
2000US-0186350.
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2000US-0229344
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                                                                                                                             (first entry)
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3-AUG-2000;
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                                                          RESULT 7
                                                                      AAS27053
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
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                                                                                                                                                                 2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                   2000US-0250160.
2000US-0250391.
                                                                                                                          2000US-0251479
2000US-0251856
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20000S-0249299
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                                                                                                                                                                                                                               WPI; 2001-465460/50.
P-PSDB; AAU17136.
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01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
06-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
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08-DEC-2000; 2
     17-NOV-2000;
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The invention relates to novel isolated polypeptides (1), and diagnosing, preventing and treating diseases including immune system diagnosing, preventing and treating diseases including immune system diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, primary hemantopolitic disorders, in mary haematopolitic disorders, myeloproliferative disorders (e.g. Alzhelmer's disease, Parkinson's disease), chromosomal aborders (e.g. Alzhelmer's disease, Parkinson's disease), chromosomal aborders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (inflammatory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disorders), liver disorders (clrihosis), astimulators of Breali responsiveness to pathogens, activators of a stimulators of Breali responsiveness to pathogens, activators of the invention 61 GCCCGCTGCCCGCCCGCAGTTCCCCGGCCCCCCCCCCAGTCATGGCGAAGCAGTACGA Gaps pathway protein coding sequences and PCR primers of the invention 22; Length 2021; ő 35.6%; Score 1160.6; DB 22; Lengt 99.2%; Pred. No. 1.8e-271; tive 0; Mismatches 9; Indels Best Local Similarity 99.2 Matches 1166; Conservative ~

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1177 1081 1117 1057 1021 997 841 877 901 937 961 637 661 697 721 757 781 421 601 361 241 TGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGGCCAAAACCCGAGGGCCCCAGCGAACTC TICGAAAACCIGCIGGIGCIGAGICCIGIGIGGGGCACCCCACACGACACCCCTCIICCC TGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGTCTTCTTCAG CCTGTTTCCCCAGCCAGCCTGCTACGACCCCCACGATGTGCCGCAAGCACTGTCTCA CCATCCCGCACCACCAGACAACAGCCAGGCTGGAGTCCAGGCCACTTTCAGCTGCTCC GACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCGGTCCCCGTGTGTC GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT AGAGCTGGTGCTGCAGGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAA CCGCTTCACCGACAACGAGTTCCACTCCTCGCACCATCTCCACCGTCGTTTGACTTTAA CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA CTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGAC GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG CTGCTGTGTGCAGCTCGCTCTTTCCTTCCTTCCTA 1176 1142 542 578 602 638 662 869 722 758 782 818 902 962 362 422 458 158 218 242 278 302 338 398 482 122 182 음 g 셤 á g ŏ 셤 ò ద ö 쇰 à g ŏ g δŏ g ö g δ g δ 셤 ă 셤 ò ద ŏ 셤 δ 셤 ð 97

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us-09-817-198b-1.rng

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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
                                                                                                      2958 CCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3078 GCACGCCACCIGCICCIGAGCCICCACIAICICCCIGIGACGGGTGAACIICGIGIACIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3138 TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAACACAGATGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; ss;
                                             2598 TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGA
                                                                                                                                                                                                                                                                                                    2838 GGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCAT
                                                                                                                                                                                                                                                                                                                                                                    2898 GACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding novel signal transduction pathway protein, Seq ID 507.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2538 AAAGGAGACAGCTAACTCTAGGATGAAGCTGTAGGCTGGAGTTGCTTCCTTGAAGA 2597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel polypeptide fragments (I) and the polynuclectides (II) that encode them that are highly expressed in a human bladder tumour and which have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of bladder cancer, to directly treat this form of cancer (including expression from gene therapy vectors) or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AS443260-243309 represent expressed sequence tag (BST) fragments isolated from a human bladder tumour CDNA library which encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAAACCTTTCCT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences expressed in bladder tumor tissue, and derived polypeptides, for treatment of bladder tumor and identification of therapeutic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2418 CCTGACTTACCAAACCAGGAAAACAGCAGGAGAGGGTGGCTCAGGACTTAGGGACAGGGT
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                                                                                                                                                                Expressed sequence tag; human; bladder; tumour; cancer; cytostatic; treatment; gene therapy; EST; ss.
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Pred. No. 3.8e-200;
0; Mismatches 3; Indels 1;
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                                                                                                                                     Human bladder tumour cDNA library derived EST 12.
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                                         AAZ24400 standard; cDNA; 895 BP.
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ilarity 99.5%;
Conservative
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Matches 8799
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Ruben SM;
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17-JAN-2001; 2001WO-US01312
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08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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ABK44752 standard; cDNA; 481

RESULT 10

ABK44752

ABK44752;

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The invention relates to novel isolated polypeptides (I), and polymention relates to novel isolated polypeptides (I), and treating diseases including immune system disponsing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, heamoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary hemantopolitic disorders, inperproliferative disorders (e.g. daucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), candiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders; in wound healing, epithelial cell proliferation, endocrine disorders (e.g. stroke) as talmilators of B-cell responsiveness to pathogens, activators of a stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency and hear and an and an as a means to induce the contact of the co
                                                                                polypeptides useful for diagnosing, treating, preventing and/or saing disorders related to the proteins, including cancers, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathway protein coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                                        Claim 1; SEQ ID No 507; 880pp; English.
                                                                                                                                                            disorders and neuronal disorders
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CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA 181 GCAGAAACGCCAGCTGGGAAGAGGAGCAAGGGCAGCTGGCGAAGGAGTATGGCATGGA 481 148 GCAGAWACGGCAGGTGGGAAGAGAGCAAGGGCAGCANCTGGCGAANGAGTATGGCATGGA 507 540 2 GCCCGCTGCCCGCCCGCCGCTGCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA 28 GCCCGCTGCCCGCCGCCGCTCCCGGCCCCCCCCCCAGTCATGGCGAAGCAGTACGA GATGAAGACCATAGAGGTAGACGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG | GGTCTATGACATTAGCAGCGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT 328 GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT 0; Gaps CTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGA Length 566; 4; Indels 16.4%; Score 534.2; DB 22; 98.9%; Pred. No. 1.3e-119; ive 2; Mismatches 4; Best_Local Similarity 98.9 Matches 533; Conservative 62 182 122 242 302 362 122 88 Query Match ŏ 셤 ò 셤 ð ద ò g ö 셤 ŏ g ò g δ 셤

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of ABK4460-ABK46237 represent coding sequences of human colon tumour propertion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2762 GGTGCCATTCATTGTCTTTCTCTCTAGCCCCCTCAGGAAAGAAGGACTATATTTGTACT
                                                                                                                                                                                                                                                                                                                                                                                                      useful as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2582 GTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2642 CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2702 TATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAGATCAGGCAG
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0
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Pred. No. 7.4e-106;
0; Mismatches 3; Indels 0;
                                                                                                colon tumour; vaccine; colon cancer; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 481 BP; 111 A; 113 C; 130 G; 125 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                      colon cancer polypeptides and polynucleotides,
                                                                       SEO ID
                                                                                                                                                                                                                                                                                                                                               Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 303; 147pp; English.
                                                                                                                                                                                                                                                                                                                                               Secrist
                                                                     cDNA encoding colon tumour protein,
                                                                                                                                                                                                                                                                                                                                             Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.78;
                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.48;
                                                                                                                                                                                                                            31-JUL-2001; 2001WO-US24218
                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                             Meagher MJ,
                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-241739/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                  1mmunotherapy;
                                                                                                                                           Homo sapiens
                                         05-JUN-2002
                                                                                                                                                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                             King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            supplied
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1090 CTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCC 3149
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                                                                                                         GTTAAGCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCTGTTGAGA 3061
       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                 GGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACT
                                        TATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAG
                                                                                                                                                                                                                                                   Thyroid cancer related gene sequence SEQ ID NO:5329.
                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000US-233133F.
18-SEP-2000; 2000US-233617P.
20-SEP-2000; 2000US-234034P.
20-SEP-2000; 2000US-234034P.
R 20-SEP-2000; 2000US-234509P.
R 22-SEP-2000; 2000US-234509P.
C 20-SEP-2000; 2000US-234509P.
                                                                                                                                                                                            .992/c
ABL66992 standard; DNA; 463 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-235711P.
2000US-235720P.
2000US-235840P.
                                                                                                                                                                                                                                                                                                                                                           30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-235638P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-236842P
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                          3062 C 3062
                                                                                                                                                                                                                                                                                                                            40200194629-A2
                                                                                                                                                          C 481
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27-SEP-2000;
27-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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25-SEP-2000;
                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                    15-MAY-2002
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the teatment of cancer such as colon, breast, stomach, lung, thyroid, cospophageal, ovarian, kidney, prostate or pancreatic cancer, cancer, adenocarcinoma, carcinoma, clear cell cancer, infilitrating ductal cancer, infilitrating ductal cancer, in the carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2790 CCCCCTCAGGAAAGAAGGACTATATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAAC 2849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2970 GGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGCTCTGCTGGCCCTGTTTAC 3029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 GGIGGCCIGGGGTAIGTCITGAGCCCCAGACTGTTAAGCAGGTTCTGCTGCCGGCCTGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 CCCCCTCAGGAAGAAGAAGAACTATATTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2850 ATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 GTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAG-TACGCTCACCCTAAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2910 GTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 463 BP; 116 A; 108 C; 110 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 438.8; DB 24
Pred. No. 1.7e-96;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 5329; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter KC,
29-SEP-2000; 2000US-236891P.
02-OCT-2000; 2000US-237172P.
02-OCT-2000; 2000US-237173P.
02-OCT-2000; 2000US-237294P.
02-OCT-2000; 2000US-237294P.
02-OCT-2000; 2000US-237316P.
03-OCT-2000; 2000US-237425P.
03-OCT-2000; 2000US-237456P.
03-OCT-2000; 2000US-237606P.
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99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Augustus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-188264/24
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young PE,
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334

2969

3089

241 GGCCCAGACTGTTAAAGCAGGCTCTGCTGGTTAACCGCGCCTGTTAACCTGGC 300

3052 IGTCTTGAGACTCCATCC 3069

2992 GGCCCAGACTGTTAAGCAGGCTCTGCTGGCTGTTTACTCGTCACCACCTCTGCACCTGC

240

2931

2871

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2812 TATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGAC 2872 TGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAGGTATGGGAGCAGAAGGAATT 121 TGATAGGCCCTATCCACAAGGCCCATGACTGGGAAAAGGTATGGNAGCAGAAGGAGAATT 2932 GGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGGCATGTCTTGA

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double-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in AAT19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
CS 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
cs is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
ceferrmined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
e.g.
                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. MRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 320 BP; 74 A; 75 C; 86 G; 81 T; 4 other;
                                                                                                                    3210 TATTTCAAACCACCAAAAAAAAAAAAAAAAAA 3243
                                                                                                                                     AAT25457 standard; cDNA to mRNA; 320 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1835; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                        Human gene signature HUMGS07624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP01916.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1993;
                                                                                                                                                                                                                                                                                                       17-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995
                   154
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ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                    Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
                                                                                                                                                                                                     Human colon tumour antigen polynucleotide SEQ ID NO:1930.
                                                                                                                                                                                                                                                colon tumour metastatic antigen; diagnosis; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 313 BP; 68 A; 85 C; 85 G; 73 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 1930; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secrist
301 TGTCTTGAGACTCCATCC 318
                                                                                               ABL38341 standard; cDNA; 313
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                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2001; 2001WO-US18557.
                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000; 2000US-210899P. 20-FEB-2001; 2001US-270216P.
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harlocker SL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                  WO200196388-A2.
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                  08-APR-2002
                                                                                                                                                                                                                                                                                                                                                   20-DEC-2001
                                                                                                                                  ABL38341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang Y,
                                                                                   ABL38341
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Length 313;

DB 24;

Score 307;

Query Match

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Gaps

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2752 GATCAGGCAGGGTGCCATTCATTGTCTTTCTCTAGCCCCCTCAGGAAGAAGAAGACTA 2811

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Query Match 9.6%; Score 313.4; DB 16; Length 320; Best Local Similarity 98.7%; Pred. No. 4.1e-66; Matches 314; Conservative 0; Mismatches 4; Indels 0;

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                                                                                                                                                                                                                                                                                        1064 CCATCCAGCCCCAGGCACGCCACCTGCTGAGCCTCCACTATCTCCCTGTGACGGGTG 3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atheroic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; gene therapy; antihilammatory; antiasthmatic; antiarthritis; haemostatic; antiathatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                           240
                                                                                                                                               120
                                                                                                                                                                                                                                                                                                       241 CCATCCAGCCCCAGGCACGCCACCTGAGCCTCCACTATCTCCCCTGTGAGCGGTG 300
                                                                                     9
                                                                                                                                 1 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATGGGCCCTA
                                                                                                                                                                                           3004 TAAGCAGGCTCTGCTGCTGCTGTTTACTCGTCACCACCTCTGCACTGCTGTCTTGAGACT
                                                                                                                  2884 TCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGG
                                                                                                                                                                            2944 TGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGGCATGTCTTGAGGCCCAGACTGT
                                                                                                                                                                                                                                                            181 TAACCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGTGTTGAGACT
                                                         2824 ACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGGTGATAGGCCCTA
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human rab8 homologue-encoding cDNA, SEQ ID NO:936
Pred. No. 1.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal; vulnerary; antiulcer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA09160 standard; cDNA; 1986 BP.
                           1;
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27-APR-2000; 2000US-0560875.
            99.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
             Best Local Similarity 99.03
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                3124 AACTTCGTGTA 3134
                                                                                                                                                                                                                                                                                                                                                                  301 AACTTCGTGTD 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9-PSDB; ABB11916
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Claim 1; Page 805; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10881-ABB10341 represent nucleic acids encoding them. The sequences ABB10825-ABB00524 represent nucleic acids encoding them. The sequences ABB10825-ABB00524 represent nucleic acids encoding them. The sequences ABB10825-ABB00524 represent nucleic acids encoding the nucleotides of control and sequences analyses and methods of producing the nucleotides of polypeptides of the invention. Although novel, many of the nucleotides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to pypeptides of the invention average activities including organization activities, and hence to premain therapeutic applications. The polypeptides of the invention may have warlous activities; seem cell growth factor activity; hasmatopoissis requirates; neceptor or ligand activities; confidentiator activities; setm cell accordance acids and activities; confidence of the invention are useful for preventing treating or maniforating medical confidence in oncogenesis, cencer cell proliferation or metastasis. Depending on their biological activities; polypeptides and nucleotides of the invention are useful for preventing treating or amalicrating medical confidence in confidence (conditions), conditions (e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell customers, proliferative retinopathy, atherosclerosis, occorary heart disease, confirence in schemic and encoding them) may be used to promote wound the instant in official and fungal infections in addition to many electrical and fungal infections and ulcasis, while those with growth factor activity may be used to various confirmate at a sequence or accidental damage plus in the treatment of viral, and bused to augment or replace cells damaged by limphoid the invention.

XX sequence 1986 BP; 519 A; 545 C; 465 G; 453 T; O other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polypucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides against human ovarian antigen antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumnours of ovarian or breast origin, reproductive system (alsorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian oysts, and dysmenorrhoea), endocrine disorders, infermantory conditions (e.g., mastitis, oophoritis and cagnitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders,
                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiloflammatory; gynaecological; reproductive; gene; ss.
379 AACAAGTGTGATGTGAATGACAAGAGACAAGTTTCCAAGGAACGGGGGAGAAAAGCTGGCC
                                465 AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG
                                                   139 CTCGACTATGGAATCAAGTTCATGGAGACCAGCGCAAGGCCAACATCAATGTGGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                              Human ovarian antigen HCGMA67 cDNA, SEQ ID NO:290
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                                                                                                                                                                                                              ABQ54410 standard; cDNA; 2411 BP.
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respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the fleatification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2411 BP; 600 A; 671 C; 583 G; 547 T; 10 other;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2700)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BX Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Homo sapiens, clone IMAGE:4866926, mRNA.
BC014511
BC014511.1 GI:15680292
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BG762841
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AA631242
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BB0697415
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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ACCESSION
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SOURCE
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                               Description
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                16154066 seqs, 8097743376 residues
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Listing first 45 summaries
                                                                                                      - nucleic search, using sw model
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BM462147 AGENCOURT BE868032 601444134

BE394411 601311368 BQ707160 AGENCOURT BG827823 602752318 AI355300 qt57e05.x

HTC 19-SEP-2001

BM975016 UI-CF-ECI BE799964-601587861 BM045331 60362321 BG76908 602743340 BG7692 AGENCOURT BG697415 602661196 BG76015 602724570 BG76015 602717606 BG760315 602717606 BG766350 602734571 BG181791 601506187 BE181791 601506187 BE181791 601506187 BE181791 601506187 BE181791 601506187

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                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/ILINL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: j Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
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Location/Qualifiers
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Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4866926"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
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SOURCE Numan. ORGANISM Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1081) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Onpublished (1999) COMMENT Email: cgapbs-rémail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Plate: LickNOOD row: k column: 18 High quality sequence stop: 662. Location/Qualifiers 1. 1081 /Organism="Hemo sapiens" /Ab_xref="taxon:966" /Clone="IMAGE:5479433" /Clone="IMAGE:5479433" /Clone=lib="MXH_MGC_98" /Lib_wise="taxon:966" /Lib_wise="astrocytoma grade IV, cell line" /Lib_host="astrocytoma grade IV, cell line" /Lib_host="bill08 (phage-resistant)" /note="organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: Clone into EcoRI: CDNA made by oligo-dT priming Directionally Cloned into EcoRI: CDNA made by oligo-dT priming the fallowing Event	Canoned into Scokol/Xnot sites using the following 5' addaptor: GGCAGGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHLMGC Library. BASE COUNT 260 a 295 c 295 g 229 t 2 others Ouery Match Query Match Query Match 29.1%; Score 947.8; DB 13; Length 1081; Best Local Similarity 95.4%; Pred. No. 1.4e-153; Matches 1029; Conservative 0; Mismatches 44; Indels 6; Gaps 5; Qy 1178 GCTATCCAAGGGATGGACCCAGGCTCGGGGGGTTCCACCCTTGGATCCAGGAAGAA 1237	QY 1238 CCCTCCACCTGGCTGGGTGGGCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCA 1297 Db 61 CCCTCCACCTGTGGGTGGGCCAAAGGCTACAGGTGCTTCTTCCTCTTCCCCCA 120 QY 1298 CCCCACTGTCCCTCATGTGCCATGGGCTGCCTCCCCCAGTGACTGCGAAAGTGGAGCA 1357 Db 121 CCCCACTGTCCCTCATGTGCCATGGGCTGCCTCCCCCAGTGACCTGCGAAAGTGGAGCA 180 QY 1358 TCGAGGTAGGAAACAGCAACCGGGGAGTCCTCCGAGCTGGCTG	09 1418 CCCATTCCCCGACGAGGTTTGCCCTTGCTTGCCTGCCCTGCCTTTGGGGAACT 1477 1 1 1 1 1 1 1 1 1
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E. 1 (bases 1 to 957)

I. Onpublished (1999)

I. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Robin Library Sequence column: 12

High quality sequence stop: 555.
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              AGCTCCTATGTATCAGGTTAAGAGCAAGGGAGAGCTGGCCAGGGACAGCAGTTTGCACAG
                                                                                     541 AGCTCCTATGTATCAGGTTAAGAGCAAGGGAGAGCTGGCCAGGGACAGCAGTTTGCACAG
                                                                                                                 1778 CAGAGGGGAATGTAGCAACAGCAGGGCCTCCTAGGCCCCCATCTTCCATTTCTTAGGTAAG
                                                                                                                                                                               AAGAGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGCCTAGGCCTTCAGCAACCAAGGTT
                                                                                                                                                                                              781 GGCCTGNGTAGAAACGCTTGGTGCTGTTCTCTTTGGCCTTT-AGACAAAGCGCTCATCTT
                                                                                                                                                                                                                                                                                                                                                            GCCCTCTACCTCCTGATAGGCTTGAGGGTTTGCCAACCACACTGTGGCTACAGGTGGAGG
AGTGACACTGTCAGGCCAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACT
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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/clone="IWAGE:6482195"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' dabptor: GGCAGCAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library.
39 a 251 c 266 g 199 t 2 others
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Pred. No. 9.2e-138;
0; Mismatches 22;
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1374 ACAGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAG 1433
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Homo sapiens cDNA clone IMAGE:6061422
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NIH-MG http://mgc.ncl.nih.gov/.
National institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                         601 CCAAGGCCTGTGGGTACTCCAGGGCAAGGAGGCCCTGNGGTCAGTGACACTGTCAGGC
    121 CGTGTGTCTGCTGTGTGCAGCTCGCTCTTTCCTTCCTTAGCTATCCAAGGGGATG
                                                                                              1194 GACCCAGGCTCGTGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTC
                                                                                                                    181 GACCCAGGCTCGTGGGAGGTTCCACCTTGGATCCAGGAAGAACCCTCCACCCTGCCTC
                                                                                                                                                                                                                                        241 GTGGGTGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCACTGTCCCTCA
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AGENCOURT_7594485 NIH_MGC_72
5', mRNA sequence.
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E 1 (bases 1to 908)

I Unpublished (1999)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (Consortium (LINL))

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

I column: 22

High quality sequence stop: 638.

Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6187941"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%; Score 840.2; DB 14;
larity 97.6%; Pred. No. 4.9e-135;
Conservative 0; Mismatches 19;
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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cuba. Library Preparation: Life Technologies, Inc.
cDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM1331 row: e column: 07
High quality sequence stop: 666.
High quality sequence stop: 666.

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                         Tissue Procurement: AICC/DCID/DIP
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/clone_lib="NIH_MGC_7"
/tissue_type="small_cell carcinoma"
/tissue_type="small_cell carcinoma"
/tissue_type="small_cell carcinoma"
/cell_line="MGC_7"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lulug; Vector: pOTB7; Site_1: XhoI; Site_2:
FCORI: CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
50 a 225 c 244 g 195 t
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Mammalia; EutoPia; Primates; Catarrhini; Hominidae; Homo.
(base; 1 to 924)

National Institutes of Health, Mammalian Gene Collection (MGC)
(contact: Robert Strausberg, Ph.D.
(Contact: Robert Strausberg, Ph.
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                                               CTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGC
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Pred. No. 2.2e-128;
0; Mismatches 54; Indels 4;
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/db_xref="taxon:9606"
/clone="IMAGE:5015713"
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/tissue_type="teratocarcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/note="Organ: ovary: Vector: poTB7; Site_1: EcoRI; Site_2:
Xhoi; cDNA made by oligo-dr priming.
Into EcoRI/XhoI sites using the following 5' adaptor:
aboratory of Gerald M. Rubin (University of California,
Berkeley) using 2AP-CoNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                Conteact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://mage.llnl.gov
Plate: LLCM2042 row: h column: 06
High quality sequence stop: 570.
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 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                             Score 799.2; DB 14; Length 1046;
Pred. No. 5.4e-128;
0; Mismatches 23; Indels 4;
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/organism="Homo sapiens"
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/clone="IMAGE:5804597"
/clone_llb="NIH_MGC_109"
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250 c 291 g
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Best Local Similarity 96.9%;
Matches 847; Conservative (
                         Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1046)
                                              TGGGTACTCCAGGGGCAAGGAGACCCTGGGGTCAGTGACACTGTCAGGCCAACCATGCA
                                                                                    CTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGAGCA
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CODNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Apencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LiAM12275 row: i column: 15
High quality sequence stop: 607.
I. 1027
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/lab_host="DH10B (phage=resistant)"
/note="lorgan: uterus; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "1 to thers
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NIH-WGC http://mgc.nd:nih.gov/.
             CCACCGTCCCAAGGTGGGCAAGGCCTAGGAAGAGGGTCATTCTTAAGCCACACATTAGCT
TCCTTCCTCCAGAGTGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAG
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24.0%; Score 781.2; DB 13; Length
Best Local Similarity 97.9%; Pred. No. 6.8e-125;
Matches, 823; Conservative 0; Mismatches 14; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:5555414"
/clone_lib="NIH_MGC_71"
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878 bp mRNA linear EST 01-MAY-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
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62 TCTACCCATTCCCCGACCACCAGGCTTTGCCCTTGCTTGGCTGCCCGCCTGCTTTTGGGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: McCray, PB
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCWV-SPORTE; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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                       Contact (Agapbs remail inthogov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Colone distribution: MGC clone distribution information can if
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov a column: 14
High quality sequence stop: 768.
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                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4748437"
/clone=lib="NCI_CGAP_Skn4"
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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ilarity 97.4%;
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/note="Organ: Luny: Vector: pt773-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; modified polylinker; Site_1: EcoR I; Site_2: Not I; following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand oDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, dispested with Not I, and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Eax: 319 356 7171
Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                        601 ACTTACCAAACCAGGAAAACAGCAGGAGGGGGGGGCTCAGGACTTAGGGACAGGGTATAG 660
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
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                                                                                                 2542 GAGACAGCTAACTCTAGGATGAAGCTGTGACTAGG-CTGGAGTTGCTTCCTTGA-AGATG
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                                                                2482 CTTAGATGGTGGAAAGCAAAGGAGGAGGAAGTTGTAAATCACTGGCTAATGAGAAAAG
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EM977746.1 GI:19596476
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/clone="UI-CF-EN1-aef-h-15-0-UI"
/clone_lib="UI-CF-EN1"
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/organism="Homo sapiens"
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Seq primer: M13 FORWARD
POLYA=Yes.
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BM975016.1 GI:19592612
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first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG_LIB-UT.CF-ENI
TAG_TISSUE-Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
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Pred. No. 2.1e-120;
0; Mismatches 8; Indels 0;
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Best Local Similarity 99.0%;
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ò 윱 à 셤 ò 셤 ò BM975016 763 bp mRNA linear EST 21-MAR-2002 UI-CF-EC1-acf-d-07-0-UI.sl UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-acf-d-07-0-UI 3', mRNA sequence.

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ACCESSION

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/do.tare="taxon:900"
/clone="UI-CF-ECI-acf-d-07-0-UI"
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/der_en_organ: Lung; Vector: pr773-pac (Pharmacta) with a formalized CDNA library containing the UI-CF-ECI is a normalized CDNA library containing a constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oilyo-dr prime containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into prT73-Pac vector: The oilgonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the Anguereman.
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TAG_TISSUE-Normal Lung Epithelial Cells Tissue nos 369-371
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                                                                                                                                                                                                                                                                                                            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Tel: 319 356 711.
Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: Mi3 FORWARD
POLTA-YES:
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Pred. No. 8e-119;
0; Mismatches
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/organism="Homo sapiens"
                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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195 c 170 q
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                                                                                                                                                                                                                                           Contact: McCray, PB
                                                                                                                                                                                                                                                                                              University of Iowa
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                                                                                                                                                                  discovery
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/clone="IMAGE:3942230"
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/db_host="DHLOB (phage=resistant)"
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ECORI; CDNA made by Oilgo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAGG(G). Size=relected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
23 c 281 g 206 t lothers
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E 1 (bases 1 to 990)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                             2774
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                                                                                                                                                                                                    TGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGG
                                TCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGCTC
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                                                                                               GTCTTTCTCTCTCTAGCCCCCCTCAGGAAGAAGAAGGACTATATTTGTACTGTACCCTAGGGGT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                           123 GGCAACC-AGGAGTCCTCGAGCCTGGGCTGCCTACCTTACCCATTCCCCGACCAGG
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                                                                1256 GGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCCACTGTCCTCATG
                                                                                                                               1316 TGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGAAAC
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                                  12;
 Length 990;
                                  Indels
22.9%; Score 746; DB 12;
95.9%; Pred. No. 7.9e-119;
ative 0; Mismatches 25;
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us-09-817-198b-1.rst

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Homo sapiens
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Site_2: EccRI; cDNA made by oligo-dT priming.

Directionally cloned into EccRI/AhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH MCC Library.

267 c 181 g 166 t
                                                                                                                                                                                                                                                                                                                                                         BM045331 732 bp mRNA linear EST 07-NOV-2001
603623321F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5449420 5',
                                                                        CCTCCAGAGTGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAGCTCGT 2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Emall: cgapbs-r@mail.nih.gov
    Tissue Procurement: DCTD/DTP
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: The J.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
    http://image.llnl.gov
    Plate: LLCM1936 row: i column: 05
    High quality sequence stop: 724.
    Location/Qualifiers
    I. 733
    I. 733
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    //db_Xref="tamon sapiens"
    //db_Xref="tamon sapiens"
    //lssue_type="carcinoma" cell line"
    //lssue_type="carcinoma" cell line"
    //lb_bost="DH108"
    //lsb_locationma" cell line"
    //lb_bost="DH108"
    //lssue_type="carcinoma" cell line"
    //lb_bost="DH108"
    //lb_bost="DH108"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTGGAAGGCCTCCGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGA
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Gaps
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al Similarity 99.3%; Pred. No. 1.2e-114;
725; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM045331.1 GI:16774598
                                                                                                                                                                        2152 AGGAGGCCCT 2161
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AUTHORS
TITLE
JOURNAL
COMMENT
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BM045331
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BG769088 749 bp mRNA linear EST 15-MAY-2001 602743340Fl NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4873185 5',
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241 ACTCCCCCTGCCTGGCCCTGAGAGCGCTCTGCTCTCATCTCAAGCAGCCCCTGTCCCCA 300
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: ARCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCGTCCACCCTGGAGTGGTCTTCTTCAGCCTGTTTCCCCAGCCACAGGCCTGCTACGA
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                                                                                        ACTCCCCCTGCCTGGCCCTGAGGGGGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1750 row: o column: 10
High quality sequence stop: 745.
Location/Qualifiers
1. 749
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/db_xref="taxon:9606"
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EST.
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BG769088
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/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: poTB7; Site_1: XhoI;
Site_2: EcoR; Colon made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGGG). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library.

a 202 c 221 g 153 t
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                                        BMO49329 766 bp mRNA linear EST 07-NOV-2001 603626279F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452987 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGCTTTGCCCTTGCTTGGCTGCCCGCCTGCCTCTTTGGGGAACTGAGCTCAGAGGCAG 1491
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)

NIH-MGC http://mgc.ncl.nih.gov/.
Mational institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                         Email: cgapDS-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Richer Consortium/LLNL at:
Plate: LLCM1945 row: m column: 20
High quality sequence stop: 758.
Location/Qualifiers
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Local Similarity 99.2%; Pred. No. 9.3e-114;
nes 762; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:5452987"
/clone_lib="NIH_MGC_40"
                                                                                                                BM049329.1 GI:16778596
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                                                                              mRNA sequence.
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                                                          DEFINITION
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COMMENT
  RESULT 15
BM049329
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                                                                                                ACCESSION
                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                       AUTHORS
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                                /issue_irpe="melanotic melanoma, high MDR (cell line)"
/lab_host="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: porps; Site_1: xho!; Site_2:
ECORI; CDNA made by voligo-dT priming. Directionally cloned
into EcoRI/xhoI sites using the following 5' adaptor:
GGCAGGG(G). Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript.
II RT (Life Technologies). Note: this is a NIH_MGC
Library. ||
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Pred. No. 1.3e-114;
0; Mismatches 2;
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/clone_lib="NIH_MGC_49"
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Best Local Similarity 99.5%;
Matches 745; Conservative (
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Length 766; Indels 1611

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Search completed: June 23, 2003, 17:08:10 Job time: 4320 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                             OM nucleic - nucleic search, using sw model
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Title: Perfect score: Sequence:	US-09-817-198B-1 3257 1 tgcccgctgcccgccgcag,aaaaaaaaaaaaaaaaaa 3257
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	441362 segs, 153338381 residues
Total number of	Total number of hits satisfying chosen parameters: 882724
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description	Sequence 2, Appl1	'n	4	Sequence 4, Appli	10,	142	4, 7	99	28,	6, 2	14,	4, 7	8	ģ	Sequence 11, Appl	7	54,	1, 1	13,	1, 4	68,	Sequence 2, Appli	7	Sequence 2, Appli	33,	S,	Sequence 5, Appl1
SUMMARTES	QΙ	US-08-824-873-2	US-09-198-184-2	US-08-916-901-4	US-09-154-602-4	US-09-075-454-10	US-09-484-970B-142	US-08-773-423-4	US-09-399-913-66	US-08-888-077A-28	US-08-741-411-6	US-08-232-463-14	US-08-741-411-4	US-09-075-454-8	US-08-766-551-6	US-09-075-454-11	US-08-741-411-2	US-09-149-476-54	US-09-493-914-1	US-09-075-454-13	US-09-156-979-1	US-09-387-341-68	US-08-842-976-2	US-09-213-397-2	US-09-416-489-2	US-09-325-932A-33	US-08-247-946A-5	PCT-US95-06420-5
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	Score	156.6	156.6	156	156	136.2	136.2	120.6	113	110	91.2	82.8	9.08	80	80	80	79	77	75.6	73.6	71.6	71.6	67.2	67.2	67.2	66.2	64.8	64.8
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Gaps

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Length 1340;

Query Match
4.8%; Score 156.6; DB 2; Length
Best Local Similarity 59.0%; Pred. No. 8.1e-30;
Matches 305; Conservative 0; Mismatches 209; Indels

Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 150, Appl Sequence 14, Appli Patent No. 5378464 Sequence 4, Appli Sequence 2, Appli Sequence 1, Appli	
3 US-09-156-807-1 2 US-08-948-616-6 2 US-09-193-510-6 4 US-09-368-402-6 2 US-09-161-015-1 1 US-09-387-341-150 1 US-08-23-463-14 6 5378-464-1 2 US-08-766-551-4 2 US-08-766-551-4 2 US-08-766-551-4 4 US-09-154-602-2 2 US-08-773-423-6 4 US-09-713-423-6 4 US-09-713-8228-1 4 US-09-397-787-119 6 US-09-71-8228-1 6 US-08-105-1119 6 US-09-71-8228-1 7 US-08-10-1119 7 US-09-721-8228-1 8 US-09-721-8228-1 1 US-08-300-9038-8	ALIGNMENTS 117 117 118 119 119 119 119 119 119 119 119 119
61.2 1.9 1098 60.6 1.9 1098 60.6 1.9 1098 60.4 1.9 1284 60.4 1.9 1284 60.4 1.9 1284 55 1.8 2918 55 1.8 2918 54.6 1.7 1334 56.2 1.6 624 50.2 1.5 227 50.2 1.5 227 50.2 1.5 1155 624 6 1.7 1334 7 49.8 1.5 13155 8 49.8 1.5 13155	1. 1. 684-873-2 ence 2, Appl ERAL INFORME PPLICANT: EPLICANT: ELECOMMUNICATIONE: ELECOMUNICATIONE: ELECOMMUNICATIONE: ELECOMUNICATIONE: ELECOMMUNICATIONE: ELECOMMUNICATIONE: ELECOMMUNICAT
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Pred. No. 8.1e-30;
0; Mismatches 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08916901
Patent No. 5892012
SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCNOTO4
CLONE: 738957
                                                                                                                                                                                                                Query Match
Best Local Similarity 59.0%;
Matches 305; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STATE: CA
COUNTRY: USA
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                                                                                                                                                                     US-09-198-184-2
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                                                                                                                                                                     174 GACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGAC
                                                                                    CTGTGC-CGCTTCACCGACAACGAGTTCCACTCGCACATCTCCCACCATCGGTG--TT
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0240 US
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/198,18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09198184 Patent No. 6010859 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
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56.7%; Pred. No. 9.7e-30;
ive 0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                          COMPUTER READBLE: FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: TEM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
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  APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TILLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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Best Local Similarity 56.73
Matches 288; Conservative
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CLONE: 2514506
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Pred. No. 9.7e-30;
0; Mismatches 220; Indels
SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                        APPLICATION NUMBER: US/08/916,901
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Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                             FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.7
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: LIVRIUT04
CLONE: 2514506
                                                                                                                                            APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TACGACCTCACGGCAAGGTGATGCTTCTGGGAGACACAGGCGTCGGCAAAACATGTTTC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 CTGTGCCGCTTCACCGACAACGAGTTCCACTCCT---CGCACATCTCCCACCATCGGTGTT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 CTGATCCAATTCAAAGACGGGCCCTTCCTGTCCGGAACCTTCATAGCCACCGTCGGCATA 210
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                                                                                             312 TIGCITCIGCIGIAIGACAICACAACAACAATCITICGACAACAACAACAGGCCTGGCTC 371
                                                                                                                                                                                                                          AGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCT 413
                                                                                                                                                                                                                                                                                                    414 GATGAGGAGCAGAAACGGCAGGTGGGAAGAGAGCAAGGGCAGCAGCTGGCGAAGGAGTAT 473
                                                                                                                                                                                                                                                                                                                            372 ACTGAGATTCATGAGTATGCCCAGAGGACGTGGTGATCATGCTGCTAGGCAACAAGGCG 431
                                 192 GACTICAGGAACAAGGIGGIGACIGIGGAIGGCGIGAGAGGIGAAGCIGCAGAICIGGGAC 251
                                                                       234 ACTGCAGGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 GACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGAC
                                                                                                                                                   294 ATATTTTGGTCTATGACATTAGCAGCGGCTCTTACCAGCACATCATGAAGTGGGTC
174 GACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 412477.1CB1
US-09-484-970B-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 136.2; DB 4;
Pred. No. 1.5e-24;
0; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142, Application US/09484970B
Patent No. 6426186
GENERAL INPORMATION:
APPLICANT: VOLKMUth, Wayne
APPLICANT: Walker, Michael G.
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%;
Best Local Similarity 57.5%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-484-970B-142
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Pred. No. 8.9e-25;
0; Mismatches 193;
                                                                                                                                                                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neal C.
APPLICANT: Patterson, Chandra
APPLICANT: Baughn, Marlah R.
TITLE OF INVENTION: RAS PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DILVE
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE, POCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                       516 ATTAAAGAGTCATTCACGCGTCTGACAG 543
                                                                                           537 GTCGAGCAGGCGTTCATGACCATGGCTG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: WORD Perfect 6.1/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,454
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILLING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        Sequence 10, Application US/09075454
Patent No. 6391580
                                                                                                                                                                                                              10:
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4.2%;
Best Local Similarity 57.5%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: ' 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: UCMCL5T01
CLONE: 1528559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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US-09-075-454-10
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    420 CGATCGTCGTCGTCGTCGTGACAAAGTGACCTCAGCCAGGGCCGGGAAGTGCCCA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261
                                                                                                                                                  262 TCACAAAGCAGTACTATCGGCGGCCCAGGGGATATTTTGGTCTATGACATTAGCAGCG 321
                                                                                           240 GCACCGCTGTCAAGGCTCAGATCTGGGACACACAGCTGGACCGGGGTACCGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Ping
APPLICANT: An, Wengian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
TITLE OF INVENTION: POTASSIUM CHANNER: US/09/399,913
CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER APPLICATION NUMBER: USSN 09/298,731.
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
                                                                 202 ACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGGGCAGGAGAGATACCAGACCA
                                                                                                                                                                                          300 TCACCICGGCGTACTATCGIGGIGCAGIGGGGGCCCTCCIGGIGITIGACCTAACCAAGC
                                                                                                                                                                                                                                   322 AGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAG
                                                                                                                                                                                                                                                                             360 ACCAGACCTATGCTGTGGTGGAGGGATGGCTGAAGGAGCTCTATGACCATGCTGAAGCCA
                                                                                                                                                                                                                                                                                                                  382 GCGICCAGAAGAICCITAITGGGAATAAGGCIGAIGAGGAGCAGAAACGGCAGGIGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                       442 GAGAGCAAGGCAGCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 113; DB 4;
Pred. No. 5.2e-19;
; Mismatches 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66, Application US/09399913
Patent No. 6361971
GENERAL INFORMATION:
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52.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Best Local
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60 TGCGGANCAAGATGGGAATGGAACTGAGGAAGATTATAACTTTGTCTTCAAGGTGGTGC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 TGATCGGCGAATCAGGTGTGGGGAAGACCAATCTACTCTCCCGGATTCACGCGCAATGAGT 179
                                                                                                    451 GATATGAGCAGCGAAAGAGTGATCCGTTCCGAAGACGGAGAGCCTTGGCCAGGGAGTAC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 TCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAG 201
                                                             GATGAGGAGCAGAAAACGGCAGGTGGGAAGAGAGCAAGGGCAGCAGCTGGCGAAGGAGTAT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TCCCGGCCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGC
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                                                                                                                                                                      GGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 3.7%; Score 120.6; DB 2; al Similarity 51.5%; Pred. No. 7.3e-21; 301; Conservative 0; Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: - US/08/773,423
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         Hillman, Jennifer L.

APPLICANT: Goli, Surya K.

APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0183
                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08773423 Patent No. 5869291 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 847 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                              474
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Matches 30
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LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 236; Conservative
INFORMATION FOR SEQ ID NO:
                 SEQUENCE CHARACTERISTICS
                                                                                          linear
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                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTC 530
                                                                                                                                                                121 GTAGAGTTTGGTGCTCGAATGATAACCATTGATGGGAAACAGATAAAACTCCAGATCTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AGTGACTTAGAATCTAGGAGAAGTGAAAAGGAAGAAGGTGAAGCTGTTTGCACGAGAG 420
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61 TGCTTATTGCTACAGTTTACAGACAAGAGTTTCAGCCGGTGCATGACCTCACAATTGGT
                                                                                                                                                                                                    GACACTGCAGGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAG
                                                                                                                                                                                                                                                                              291 GGGATATTTTGGTCTATGACATTAGCAGCGCGCTCTTACCAGCACATCATGAAGTGG
                                                                                                                                                                                                                                                                                                               241 GGGGCTTTACTAGTGTATGATATTACAAGGAGAGACACGTTCAACCACTTGACAACCTGG
                                                       111 TGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGT
                                                                                                                               GTTGACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGG
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APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMANNS, JOHANNA M
APPLICANT: ROMANNS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENEFIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: LENNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/TOCKET NUMBER: SCHERING
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,077A
FILLING DATE: 03-JUL-1997
CLASSIFICATION: 530
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
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COMPUTER READABLE FORM:
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US-08-888-077A-28
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                                                                                                                                                                                                                  55 AGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCC 114
                                                                                                                                                                                                                                                                    73 AGTACGACTACCTCTTTAAAGTTGTCCTTATTGGAGATTCTGGTGTTGGAAAGAGTAATC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 CAGCAGGCCAAGAGCGATATCGAGCTATAACATCAGCATATTATCGTGGAGCTGTAGGTG 312
                                                                                                                                                                                                                                                                                                                  115 TGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTG 174
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                                                                                                                          Length 970;
                                                                                                                     Score 110; DB 3; Length 97
Pred. No. 3.6e-18;
0; Mismatches 210; Indels
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STREET: 3174 PORTER Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bar Young, Janice
TILLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 GCATGGACTTCTATGAAACAAGTGCC 500
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,411
FILING DATE: Herewith
; MAME/KEY: misc_feature
; LOCATION: 1..970
; OTHER INFORMATION: /note= "Y2H9"
US-08-888-077A-28
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: 1800 Diagonal Road, Suite 500 Alexandria
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                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                        NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                        CLASSIFICATION: 435
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US-08-232-463-14
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                                                                  22313-0299
                                                      USA
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US-08-741-411-4
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Pred. No. 1.8e-13;
0; Mismatches 203; Indels
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Fatent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                     PF-0139 US
                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%;
Best Local Similarity 52.3%;
Matches 226; Conservative (
                                                             ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                    FILING DATE:
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US-08-741-411-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7218;
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8.3%; Pred. No. 1.1e-11;
ve 251; Mismatches 123; Indels
                                        SOFTWARE: PALENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1420 YYYYYYYYYYYYYGTACCAAA 1442
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                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.3%; Sc
Best Local Similarity 2.3%; Pre
Matches 9; Conservative 251;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                   29,768
                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Query Match
Best Local Similarity
Matches 161; Conserv
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LIBRARY: KIDAL
627565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                             US-09-075-454-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-075-454-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GACTCCGGGGTGGGCAAGACCTGCCTGTGTGCCGCTTCACCGACAACGAGTTCCACTCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 TCGCACATCTCCACCATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCATC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AAGCAGTACTATCGGCGGCCCAGGGATATTTTTGGTCTATGACATTAGCAGCGCGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 CGAGTATACTACAAGGAAGCTGTTGGTGCTTTTGTAGTCTTTGATATATCAAGAAGTTCC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 ccecceccada de la constante de la constante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 TCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGAT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 ACATTTGAGGCAGTCTTAAAATGGAAAAGTGATCTGGAT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                           APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bar-Young, Janice
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 80.6;
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SOCTWARE: FRSTSEQ Version 1.5
CURRENT APPLICATION DATA: 08/08/741,411
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
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TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus
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                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
Patent No. 6124116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-741-411-4
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 CTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAAGAT
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Pred. No. 1.3e-10;
0; Mismatches 135;
                                                                                                                                                                                                                                                                                             INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word Perfect 6.1/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/09/075,454
Herewith
                                                                                                                                                                                         APPLICANT: Batra, Sajeev
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: DECEMBER 12, 1996 ATTORNEY/AGENT INFORMATION:
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Sequence 8, Application US/09075454 Patent No. 6391580
                                                               Hillman, Jennifer L.
                                                                                                                                                                                                                                                                     INCYTE PHARMACEL
TABLE 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTER
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                                                                                                                                               Corley, Nell C.
Patterson, Chandra
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illarity 54.4%;
Conservative (
                                                                                  Tang, Y. Tom
Lal, Preeti
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cerrone, Michael REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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598 GITCIGCAAAGACACCITIGATAAGAATTACAAGGCCACCATIGGAGTGGACTICGAGAT 657
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695 GGAGAGGTTCAAATGCATTGCATCAACCTACTATAGAGGAGCTCAAGCCATCATCATTGT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 CTATGACATTAGCAGCGGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACG 360
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Pred. No. 1.5e-10;
0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Batra, Sajeev
PAPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 POTER DI'VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0168-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09/075,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  Sequence 11, Application US/09075454 Patent No. 6391580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                           Patterson, Chandra
                                                                                                                                                                                                                              Hillman, Jennifer
                                                                                                                                                                                                                                               Tang, Y. Tom
Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.5%;
Best Local Similarity 54.4%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: PROSTUT08;
CLONE: 1651593
US-09-075-454-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palo Alto
                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Hillma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                              RESULT 15
US-09-075-454-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                     Gaps
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54.4%; Pred. No. 1.4e-10;
tive 0; Mismatches 135; Indels
                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN GTP-BINDING PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INVTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/766,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA: PRPLICATION NUMBER: US/08/766
                                                                                                       RESULT 14
US-08-766-551-6
; Sequence 6, Application US/08766551
; Patent No. 5840569
; GENERAL INFORMATION:
utilman. Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LIBRARY: SEQ ID NO:6
; CLONE: 627051
US-08-766-551-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Matches 16
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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OM nucleic - nucleic search, using sw model

Run on:

June 23, 2003, 13:39:33 ; Search time 443 Seconds (without alignments) 10788.737 Million cell updates/sec

US-09-817-198B-1 3257

Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1042519 seqs, 733713590 residues Searched:

2085038 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* Database

/ cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/ cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: ptodata/1/pubpna/US10_NEW_PUB.seq /cgn2_6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 3, Appli	~	Sequence 28, Appl		Sequence 30, Appl		Sequence 31, Appl		Sequence 303, App	ď	Sequence 20848, A	Sequence 1930, Ap	Sequence 1930, Ap	Sequence 1930, Ap	Sequence 9, Appli	Sequence 7, Appli	Sequence 879, App	Sequence 885, App
ID	US-09-817-198A-1	US-09-817-198A-3	US-09-764-868-88	US-09-817-198A-28	US-09-817-198A-29	US-09-817-198A-30	US-09-764-868-507	US-09-817-198A-31	US-09-920-300A-303	US-10-033-528-303	US-09-964-824A-26	US-09-918-995-20848	US-10-046-935-1930	US-09-878-178-1930	US-10-146-502-1930	US-09-794-257-9	US-09-794-257-7	US-09-834-975-879	US-09-834-975-885
DB	101	10	<u>ه</u>	10	10	10	6	10	10	12	10	6	σ	6	σ	10	10	10	10
% Query Match Length DB	3257	28770	2021	601	601	601	266	601	481	481	463	458	310	310	310	624	1161	2497	2497
% Query Match	100.0	82.8	35.6	18.4	18.4	16.6	16.4	15.9	14.7	14.7	13.5	13.0	₽.6	9.4	9.4	6.7	6.7	6.7	6.7
Score	3257	2696.6	1160.6	599	599	540	534.2	516.6	477.4	477.4	438.8	424.4	306.8	306.8	306.8	217.8	217.8	217.8	217.8
Result No.		7	ო	₹	S	9	7		σ	. 10	c 11	12	13	14	15	16	17	18	19

Sequence 894, App Sequence 32, Appl Sequence 31, Appl Sequence 31, Appl Sequence 5605, App Sequence 5605, App Sequence 22915, A Sequence 10145, A Sequence 10145, A Sequence 10145, A Sequence 1045, App Sequence 5566, App Sequence 5566, App Sequence 44, Appl Sequence 41, Appl Sequence 71, Appl Sequence 646, Appl Sequence 10, Appl Sequence 646, Appl Sequence 646, Appl Sequence 10,	
10 US-09-834-975-894 10 US-09-834-975-896 110 US-09-917-1908-32 110 US-09-925-300-631 110 US-09-938-842A-836 9 US-09-938-842A-836 9 US-09-918-995-5605 10 US-09-918-995-22915 9 US-09-918-995-22915 9 US-09-918-995-22915 9 US-09-918-995-22915 10 US-09-918-995-22915 10 US-09-918-995-566 11 US-09-918-995-566 12 US-10-031-986-10 10 US-09-918-995-1085-995-1085-995-1085-995-995-995-995-995-995-995-995-995-9	
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217.8 217.8 210 198.4 115.3.4 115.3.4 115.3.4 115.6 11	
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ALIGNMENTS

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121 GCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCCCCACCATCGGTGTTGACTTTA 180
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          Sequence 1, Application US/09817198A
Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCCCGCTGCCCGCCCGCCAGTTCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACG
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 3257; Conservative
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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US-09-817-198A-1
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CGTGGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCCACCCCACTCTCCCTC
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                                                                                                                     TCTTTCTCTGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCGTCCC
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                                                                                                                                               TGCCAGCAATGAGTTGGCACTGGCAGAGGAGGAGGAGGAGGCCAAACCCGAGGGCCC
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                                                        Gaps
                                                      ö
                                      Length
                                                      Indels
                                     10;
                                                      34;
                                      8
                                   Score 2696.6;
Pred. No. 0;
0; Mismatches
                                    82.8%;
98.8%;
                                             Best_Local Similarity 98.8
Matches 2717; Conservative
          Human
   ; TYPE: DNA
; ORGANISM: Hur
US-09-817-198A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTIGCTICCTIGAAGAIGGGACICCTIGGGTATCAAGACCIAIGCCACAICACACIGGG
                                                                                 GCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTT
                                                                                                                    ATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAGATCAGGCA
                                                                                                                                                       CTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTA
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                                   ATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTGG
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Patent No. US20020146758A1

GENERAL INFORMATION:
APPLICAMY: YE. Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERRACE: CLOO1188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO
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US-09-817-198A-3
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Db 27602 AGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGAC 27661 Qy 2573 TAGGCTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATC 2632	QY 2633 ACACTGGGGCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCT	QY 2693 GAGAAGITAIAITGGGCAGTGGCTCCAATCIGTGGACCAGTAITTCAGCITICCCTGAAG 2752	QY 2753 ATCAGGCAGGGTGCCATTCATTGTCTTTCTCCTAGCCCCCTCAGGAAAGAAGGACTAT 2812	QY 2813 ATTGTACTGTACGTAGGGGTTCTGGAAGGAAACATGGAATCAGGATCTATAGACT 2872	OY 2873 GATAGGCCCTATCCACAAGGCCATGACTGGGAAAAGGTATGGGAACAGGAGAATTG 2932	QY 2933 GGATTTTAGGGTGCAGCTACGCTCAACCTTTTGGTGGCCTGGGGCATGTCTTGAG 2992	QY 2993 GCCCAGACTGTTAAGCAGGCTCTGCTGGCCTGTTACTCGTCACCACCACCTCTGCACTGCT 3052	QY 3053 GTCTTGAGACTCCATCCAGGCACGCCACTGCTCCTGAGCCTCCACTATCTCC 3112 Db 28142 GTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCTGAGCCTCCACTATCTCC 28201	QY 3113 TGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATGAATTGTGAGCAGGGTT 3172	OY 3173 CATCTATTTTAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCACC 3223	RESULT 3 US-09-764-868-88 ; Sequence 88, Application US/09764868	<pre>; Patent No. US20020168711A1 ; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies</pre>	; FILE REFERENCE: PT232; CURRENT APPLICATION NUMBER: US/09/764,868; CURRENT FILING DATE: 2001-01-17; Prior application data removed - refer to PALM or file wrapper		sue	Query Match 35.6%; Score 1160.6; DB 9; Length 2021; Best Local Similarity 99.2%; Pred. No. 0; Matches 1166; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	OY 2 GCCGGTGCCGGCAGTTCCCGGCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA 61
16522 GAGCTTTGCCCTTGCTTGGCTGCCCGCCTCTTTGGGAACTGAGCTCAGAGGCAGG 26581 1493 TGCTTCAGAAAGAAAAATGAGGGTGCCAGGGATAAAAAAGTCACCTCCTTCTTTGGGAACTCACCTCCATTCTTTTGGGAACTCACTC		CAGG	1673 CCAACCATGCACTCCACAAAGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCA 1732 	1733 GGTTAAGAGCAAGGGAGGCCAGGGACAGCAGCTTTGCACAGCAGGGAATGTAG 1792 	1793 CAACAGCAGGCCTCCTAGGCCCCATCTTCCATTTCTTAGGTAAGAAGAGCATTTCCTCA 1852 	1853 GACTCCCAGGCGGAGGACTGAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCAAA 1912 	1913 GTTTATGGGAGAAGGCAAAGACTTCATGGGAAGAGAAGGAAG	CTACCTC	111C	STA 	2153 GGAGCCCTTTAAAGACGGAACAAGTAATTTACCAGTTCTACTGGGGTTCCTGCCCACCG 2212 	2213 TCCCAAGGTGGGCGAGGCCTAGGAAGAGGGTCATTCTTAAGCCACACATTAGCTGCACTG 2272 	2273 CGTGGCTGCAGAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAAT 2332 	2333 CCAGGGCACTCATATGTGAAGGATAAGAACCTCACTTCCTTACTCCTCCAAAAGAAGTG 2392 	2393 GGGAAAGAACCATCAAACCTTTCCTCGACTTACCAAACCAGGAAAACAGGAGGG 2452 	2453 GTGGCTCAGGACTTAGGGACAGGTATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGA 2512 	513 AGTTGTAAATCACTGGCTAATGAGAAAAGGAGACACCTAACTCTAGGATGAAGCTGTGAC

us-09-817-198b-1.rnpb

		OV 1142 CTGCTGTGTAGCTGCTCTTTTTTTTTTTTTTTTTTTTTT
δ d	62 TGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGAAGACCTGCCTG	Db 1178 CTGCTGTGTGCAGCTCGCTCTTTCCTCTGACTTA
oy 1	22 CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA	RESULT 4 US-09-817-198A-28
8 8	135 CUGUTICACUGACAAUGAGTICCACICCICGCACATUGCICGGTGGTGGTGGTGAA 21/ 182 GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 241	; Sequence 28, Application US/09817198A ; Patent No. US20020146758A1 ; GENERAL INFORMATION:
qa	218 GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 277	AFFLICANT IE, JOHN CL AL. TITLE OF INVENTION: SOCIATED HUMAN RAS-LIKE PR TITLE OF INVENTION MICHEL ACTD MOLECHIES EN
oy Og	242 GCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT 301 	; TITLE OF INVENTION: PROTEINS, AND USES THEREOF; FILE REFERENCE: CLOO1188 ; CURRENT APPLICATION NUMBER: US/09/817,198A
oy GB	302 GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT 361 	; CURRENT FILING DATE: 2001-03-27; NUMBER OF SEQ ID NOS: 33; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 28
oy Op	362 GGATGAGTACCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 421 	S
Oy Dp	422 GCAGAAACGGCAGGTGGGAAGAGAGCAAGGGCAGCAGCAGAGGAGTATGGCATGGA 481 	Query Match 18.4%; Score 599; DB Best Local Similarity 99.7%; Pred. No. 1.1e-Matches 599; Conservative 1; Mismatches
yo, da	482 CTTCTATGAAACAAGTGCCTGCACCAACATTAAAGAGTCATTCAGGGGTCTGAC 541 	월드달
Qy Dp	542 AGAGCTGGTGCTGCAGGCCCATAGGAAGGGCTGGAAGGCCTCCGGATGCGTGCCAGCAA 601	Qy 1136 TGTGTCTGCTGTGTGGAGCTGGTCTTTCCTTCCT
oy Oy	602 TGAGTTGGCACTGGCAGAGCTGGAGGAGGGGCAAACCCGAGGGCCCAGCGAACTC 661 	Oy 1196 CCCAGGCTCGTGGGGAGGTTCCACCTTGGATCCAC
oy Og	662 TTCGAAAACCTGCTGGTGGTGGTGGGGCACCCCACACGACACCCTTTCCC 721 	QY 1256 GGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCT
ço Qo	722 TCAGGAGGCCCGTGGGCAGACAGGGGGCTTTGCCCTGCTGCTGTCCTCTGTG 781	QY 1316 TGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGT
oy G	782 TGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCTGCCTG	QY 1376 AGCAACCGGGGGGTCCTCGAGCCTGGGGCTGCCCTF :
Oy Dp	842 TGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGTCTTCTTCAG 901	QY 1436 CTTTGCCCTTGCTTGCCTGCCTGCCTCTTTG
oy Og	902 CCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCAGGATGTGCCGCAAGCACTGTCTCA 961	Qy 1496 TTCAGAGAAGGAAACAAAATGAGGGGTGGCAGGAY
Oy Og	962 CCATCCGCACCCACCAGACAACAGCCAGGGTGCAGGCCACTTTCAGCTGCTCC 1021	Qy 1556 TCCCATGCAGGATGAACACAATTTCTCTCCACCTGC
o S	1022 TTTCTCCGTGCATCGTGTTTTTTTGTCTCTCCCCCACTTCTTTTCTTT 1081	Qy 1616 AAGGCCTGTGGGTACTCCAGGGGAAGGGGCCT
Qy Dp	1082 GACCCCTCCCGTGGGTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCGGTGTGTC 1141 	Qy 1676 A 1676 Db 601 A 601

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                                                                 APPLICANT: YE, Jane et al.

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT APPLICATION NUMBER: US/09/817,198A

SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 1.1e-158;
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US-09-817-198A-30
; Sequence 30, Application US/09817198A
                                 Sequence 29, Application US/09817198A Patent No. US20020146758A1 GENERAL INFORMATION:
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99.7%;
                                                                                                                                                                                                                                                           Local Similarity 99.7
nes 599; Conservative
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APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
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Patent No. US20020168711A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
                                                                                                                                                                                                                                                                                                             Query Match 16.6%; Score 540; DB 10; Length 601; Best Local Similarity 99.6%; Pred. No. 5e-142; Matches 540; Conservative 1; Mismatches 1; Indels
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2767 CATTCATTGTCTTTCTCTCTAGCCCCCTCAGGAAAGAAGAAGAATATTTGTACTGTACC
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Fatent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Weagher, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT APPLICATION NUMBER: US/09/31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                   Length
                                                                                                                                                               Indels
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                                                                                                                                   DB 10;
                                                                                                                                 Score 516.6; DB 10;
Pred. No. 2e-135;
1; Mismatches 0;
                                Windows Version 4.0
     2001-03-27
                                                                                                                                 15.9%;
99.8%;
                                                                                                                                                              Matches 516; Conservative
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LOCATION: 417, 461
 CURRENT FILING DATE: 2: NUMBER OF SEQ ID NOS: 3: SOFTWARE: FASTSEQ for W. SEQ ID NO 31
LENOTH: 601
TYPE: DNA
                                                                                      ORGANISM: Homo sapien
                                                                                                                                                Similarity
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Best Local
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APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
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Pred. No. 2.1e-140;
2; Mismatches 4;
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NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 507
                                                                                                                                                                                                                                                                                                                                    Conservative
                                        LENGTH: 566
TYPE: DNA
ORGANISM: Homo saptens
                                                                                                                                                                        OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (538)
OTHER INFORMATION: n
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US-09-764-868-507
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533; Conserv
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NAME/KEY: SITE
LOCATION: (484)
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LOCATION: (493)
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LOCATION: (563)
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US-09-817-198A-31
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Best Local S
Matches 533
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ORGANISM: Homo sapiens
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61 CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGACTTGAGAAGTTA 120
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Magagher, Madeleine Joy
APPLICANT: Wu, Jianghen
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.54761
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
                                              DB 10; Length 481;
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                                          Score 477.4; DB 10
Pred. No. 2.1e-124;
0; Mismatches 3;
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US-10-033-528-303
; OTHER INFORMATION: n = A,T,C or G
US-09-920-300A-303
                                           Query Match
Best Local Similarity 99.4%;
Matches 478; Conservative (
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Matches 478; Conservative
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LOCATION: 417, 461
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ORGANISM: Homo sapiens
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US-10-033-528-303
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REPERENCE: 682920-73
CURRENT APPLICATION WUMBER: US/60/236,033
FRICH RILING DATE: 2000-09-28
FRICH APPLICATION NUMBER: US/60/236,032
FRICH APPLICATION NUMBER: US/60/236,032
FRICH FILING DATE: 2000-09-28
FRICH FILING DATE: 2000-09-28
SRICH FILING DATE: 2000-09-28
WUMBER OF SEQ ID NOS: 583
SOFTWARE: PARCHING DATE: 2000-09-28
SEQ ID NO 26
SEQ ID NO 26
LENGTH: 463
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                                                                                                                          2642 CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTA 2701
                                                                                                                                                                                                                                                     2702 TATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAGATCAGGCAG 2761
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                                                                                                                                                                                                                                                                                      GTACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATAGGCCC
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272 TCTCTCTAGCCCCCTCAGGAAAGAAGGACTATATTGTACTGTACCCTAGGGGTTCTGG
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                                                                2824 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTA
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APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE T
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REBERBNES: 2002-11:5271
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 306.8; DB 9;
Pred. No. 2.6e-76;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020177552A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.48;
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Best Local Similarity 99.4
Matches 308; Conservative
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US-10-046-935-1930
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US-09-878-178-1930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1930
LENGTH: 310
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ATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAG
                             GTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTT
                                                                                          GGTGGCCTGGGGCATGTCTTGAGGCCCCAGACTGTTAAGCAGGCTCTGCTGGCCTGTTTAC
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| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICAMT: Hyeeq. Inc.
| TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TILLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
| FILE REPERENCE: 2011-756
| CURRENT FILING DATE: 2011-756
| PRIOR FILING DATE: 1999-01-20
| PRIOR FILING DATE: 1999-01-20
| SEQ ID NO 20848
| LENGTH: 458
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// LOCATION: (1)...(458)
// OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20848
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Matches 42
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APPLICANT: Jinng, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Becrist, Heather
APPLICANT: Gecrist, Heather
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: GEN THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 21012.527C2
CURRENT RAPLICATION NUMBER: US/10/146,502
CURRENT PILLION DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SEQ ID NO 1930
LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                         Length 310;
               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REPERROCE: 210.121. 527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILIED DATE: 2001-06-08
NUMBER OF SEC 1D NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030069180A1
GENERAL INFORMATION:
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US-10-146-502-1930
                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapien US-09-878-178-1930
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US-10-146-502-1930
                                                                                                                                                                                          SEQ ID NO 1930
LENGTH: 310
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2824 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTA 2883

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241 CCATCCAGCCCCAGGCACCCAGCTCCTGAGCCTCCACTATCTCCCTGTGACGGTG 300
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1 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGGGCCCTA
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Job time: 445 secs
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June 18, 2003, 15:23:56; Search time 71 Seconds (without alignments) 397.875 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                    Sequence:
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| SIDS2/godgata/geneseqpeeseqp-embl/AA1995.DAT:# |SIDS2/godgata/geneseqqpeeseqp-embl/AA1996.DAT:# |SIDS2/goddata//renesex//renese /SIDS2/gcgdata/geneseg/genesegp-embl/AA1998.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseqcp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqcp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqcp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqcygeneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseqcygeneseqp-embl/AA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	20, 14, 20,000	norodi noson	Novel signal trans	Human ORFX ORF1368	Novel signal trans	Drosophila melanod	Human rab8 homolog	Human ovarian anti	Lung cancer associ	Amino acid sequenc	Human Rab10 protei	Human protein sequ	
	£		AAU17136	AAB41604	AAU17555	ABB70670	ABB11916	ABP41333	AAB58196	AAB19165	AAB09979	AAB95340	
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	Query	The state of the s	401	218	188	204	213	221	246	200	200	200	
dР	Query	March	100.0	98.8	75.3	49.5	49.3	48.9	48.1	48.0	48.0	48.0	
	9100	3000	1105	1092	832	546.5	545	540	532	530.5	530.5	530.5	
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Human prostate can	Drosophila melanog	Amino acid sequenc	rotei	Canine RablO prote	_	Human RablO protei	Arabidopsis thalia	Ø	Arabidopsis thalia	Arabidopsis thalia	Zea mays protein f	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalla		_	Human Rab protein,	Novel human secret	Human polypeptide	Breast and ovarian			Arabidopsis thalia	Gene 44 human secr	Human secreted pro	Arabidopsis thalia	Drosophila melanog	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Amino acid sequenc	Human polypeptide		
AAB56993	ABB71647	AAG67154	AAB92628	AAB09982	AAB09980	AAB09981	AAG08688	AAG53945	AAG53944	AAG08687	AAG35215	AAG19220	AAG08006	ABG23365	AAG47826	AAG47825	ABG23366	AAY00919	AAU28024	AA013525	AAB58758	AAG30499	AAG30498	AAG07763	AAB34843	AAB34844	AAG10858	ABB59808	AAG30710	AAG30709	AAG45323	AAB19163	AAM39600	ALIGNMENTS	
8 21																													•	•		7 21			
218	20	20	50	20	19	13	21	21	25	25	21	21	21	70	22	23	33	50	50	22	22	20	25	50	50	50	20	70	21	22	25	227	22		
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530.5	528.5	528.5	528.5	526	523	523	519	519	519	519	513.5	510	507	506.5	501	501	501	478.5	478.5	478.5	478.5	476	476	468	467	467	466	462	457	457	457	456.5	456.5		
11:	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33		32							42		44	45		RESULT 1

AAU17136 standard; Protein; 401 AA. (first entry) 07-NOV-2001 AAU17136;

Novel signal transduction pathway protein, Seq ID 701

Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HTV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; inflammatory condition; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; acquired immune deficiency syndrome

W0200154733-A1 Homo saptens

17-JAN-2001; 2001WO-US01312,

02-AUG-2001

2000US-0179065. 2000US-0180628. 2000US-0184664. 2000US-0186350. 04-FEB-2000; 24-FEB-2000; 202-MAR-2000; 2 31-JAN-2000;

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14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-02257557.
14-AUG-2000; 2000US-0225757.
14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225681.
22-AUG-2000; 2000US-022688.
22-AUG-2000; 2000US-022688.
23-AUG-2000; 2000US-022943.
01-SEP-2000; 2000US-022943.
01-SEP-2000; 2000US-022943.
01-SEP-2000; 2000US-022943.
01-SEP-2000; 2000US-022943.
06-SEP-2000; 2000US-022943.
06-SEP-2000; 2000US-022943.
06-SEP-2000; 2000US-022943.
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06-SEP-2000; 2000US-022944.
06-SEP-2000; 2000US-022944.
06-SEP-2000; 2000US-022944.
06-SEP-2000; 2000US-022944.
06-SEP-2000; 2000US-023144.
08-SEP-2000; 2000US-0231444.
08-SEP-2000; 2000US-0231444.
08-SEP-2000; 2000US-023144.
08-SEP-2000; 2000US-023144.
08-SEP-2000; 2000US-023144.
08-SEP-2000; 2000US-023299.
14-SEP-2000; 2000US-023240.
14-SEP-2000; 2000US-023340.
                                                                                                                                                                           14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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Ruben SM; (HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC,

WPI; 2001-465460/50. N-PSDB; AAS27053.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 701; 880pp; English

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The invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune clasorders (e.g. congenital and acquired immunodeficiencies, autoimmune trapletions and graft versus host diseases. Infectious diseases (e.g. rheading disorders, inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, clasorders, inflammatities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. Alzhelmer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (long glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders, in wound healing, epithelial cell proliferation, endocrine disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17683 represent novel signal transduction gathway protein, amino acid sequences of the invention.
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02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

Shimkets RA, Leach M; (CURA-) CURAGEN CORP.

99US-0127607

11-MAR-1999;

31-MAR-2000; 2000WO-US08621.

05-0CT-2000

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NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                          IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                              0; Gaps
Query Match 100.0%; Score 1105; DB 22; Length 401; Best Local Similarity 100.0%; Pred. No. 2.1e-108; Matches 212; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                           RMRASNELALAELEEEGKPEGPANSSKTCWC 212
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective;
w uniconvulsant; osteopathic; antiparthic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
Mypotensive; dermatological; immunosuppressive; antidiabetic;
Mypotensive; antibacterial; antifungal; antitheumatic; antithyroid;
antiviral; antibacterial; antifungal; antistheumatic; antithyroid;
antiannaemic; gene therapy; cancer; proliferative disorder; hypothyroids,
w cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AlDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
w thrombosis; contraceptive.
                                                                                                                                                                      Human ORFX ORF1368 polypeptide sequence SEQ ID NO:2736.
                      AAB41604 standard; Protein; 218 AA
                                                                                                                      08-FEB-2001 (first entry)
                                                                      AAB41604;
AAB41604
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WO200058473-A2

AAU17555 standard; Protein; 188 AA.

AAU17555;

AAU17555 ID AAU1 XX AC AAU1 RESULT 3

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; categoralic; anticonvulsant; antiarthritic; immunosuppressant; immunostimilant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; categoralic and antianaemic. The sequences can be used for determining pathological conditions associated with an ORFX-associated disorder. The nucleic acids may be used to treat cancers, proliferative disorders, onlocated acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, dypertension, hypothyroidism, cholesterol ester storage, systemic lupus allocatic and antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated and antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infection, malaria, autoimmune disorders, asthma, allocated antiderial or fungal infections and antiderial or fungal infectio
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                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
N-PSDB; AAC75813.
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Neuroprotective: cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                           Novel signal transduction pathway protein, Seg ID 1120
                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01312
                                                                                                                                                                                                                                                                                                19-MAY-2000; 2000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20000S-0231414
         07-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                           02-MAR-2000;
                                                                                                                                                    Homo saplens
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4-AUG-2000;
4-AUG-2000;
4-AUG-2000;
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PR 08-58P-2000; 20000S-0233081.
PR 14-58P-2000; 20000S-023308.
PR 22-58P-2000; 20000S-0233308.
PR 22-58P-200
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 38802; 21pp + Sequence Listing; English.
                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 38802
                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                       26-MAR-2002 (first entry)
                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                    WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions -
                                                                                                                                                    pharmaceutical
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ABB70670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel isolated polypeptides (I), and display to (I) are useful for display to (I) are useful for display preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. daucher's disease and cancer), neurodegenerative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomenilopephitiis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders in wound healing, epithelial cell proliferation, endocrine disorders (e.g. arrhythmia), respiratory disorders, daraction; as attendators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a manns to induce to party and an activators of T-cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention.
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Pred. No. 6.2e-80;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                 20000S-0256719.
20000S-0251479.
20000S-0251868.
20000S-0251868.
20000S-0251869.
20000S-0251989.
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Best Local Similarity 97.6%;
Matches 160; Conservative 0
                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                         2000US-0251030.
2000US-0251988.
                                                                                                                                                                                                                                                                          05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                      2000US-0254097
                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465460/50.
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             01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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ABB70670
ID ABB7
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18

Myers EW;

Li PWD,

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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                   61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNEKSFENIVKWLRNIDEHANEDVEKMIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                              9
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                      Gaps
                                                                                                                                                                                    6
                                                                                                                                       49.5%; Score 546.5; DB 22; Length 204; 49.8%; Pred. No. 1.4e-49;
                                                                                                                                                                                      Indels
                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 LRMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESAENQERVIIDRRNQERAP----GYSKCC 203
                                                                                                                                                                                    47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB11916 standard; peptide; 213 AA.
                                                                                                                                                                 Best Local Similarity 49.83
Matches 105; Conservative
                                                                                                                                                               Similarity
                                                                                            204 AA;
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(first entry)

Claim 20; Page 276; 1963pp; English.

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; ofmentaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastusis; carcer; tumour; haematopoletic disorder; proliferation; metastusis; carcer; tumour; haematopoletic disorder; myeloid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; enlianture; duug screening; gene therapy; antilnifammantory; antisathmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytogtatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer
Human rab8 homologue, SEQ ID NO:2286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABA09160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens.
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Sequences ABA08225-ABA09574 represent 1330 NOVEL IMMUSE PLILLES, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of polypeptides in a sample, and methods of identifying compounds which is polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence of potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; have various activities; stem cell growth factor activities; immunomodulatory activity; tissue growth activity; chambotic or chemotractic or chemokinetic activities; haemostatic, thrombotic or thrombotylic activities; receptor or ligand activities; or may be invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions and arthritis), conditions, e.g., by protein or gene therapy. Such conditions arthritis), and activities of disorders, charactery dispared activities or arthritis), and acceptance or lymphoid cell conditions, e.g., appropriations arthritis), and acceptance or lymphoid cell conditions arthritis), and activities or arthritis). З Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and proliferative retinopathy, atheroscierosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used in cell cultures

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promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                         61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                121 NKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; ovary syndrome; profession disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                   7 MAKTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                    Query Match 49.3%; Score 545; DB 22; Length 213; Best Local Similarity 52.9%; Pred. No. 2.1e-49; Matches 99; Conservative 45; Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ovarian antigen HCGMA67, SEQ ID NO:2465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP41333 standard; Protein; 221 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases -
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187 SPQGSNQ 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-147878/19.
                                                                                                                                                                 213 AA;
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                                                                                                                                                                 Sequence
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(HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.

Ruben SM;

990S-0124270.

12-MAR-1999;

08-MAR-2000; 2000WO-US05918

WO200055180-A2.

21-SEP-2000.

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                                                   The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polypuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen and the use of ovarian antigen polymuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related of sorders. Succeeditions include ovarian cancer and breast cancer, and castatic tumours of ovarian or breast origin, reproductive system of disorders (e.g., infertility, disorders of pregancy, anovulation, disorders (e.g., infertility, disorders of pregancy, anovulation, disorders, infertility, disorders of pregancy, anovulation, disorders, infertility, disorders of pregancy, anovulation, disorders, infertility, disorders or pregancy, anovulation, disorders, autoimmune opportitions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune opportitis, systemic lupus erythematosus), condurated disorders (e.g., anaemia), cardiovascular disorders and unimary system disorders. Ovarian antigen polypeptides and complete ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies of dentification of individuals and in forensic analysis, and the printed sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed of the printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 WDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 KADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer associated protein; neuroprotective; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer associated polypeptide sequence SEQ ID 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.9%; Score 540; DB 23; 52.7%; Pred. No. 7.5e-49; ive 45; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
               SEQ ID No 2465; 2922pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58196 standard; Protein; 246 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA;
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               Claim 11;
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polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; expostatic; cardioactive; antagonists may have neuroprotective; cytostatic; cardioactive; antagonists may have neuroprotective; cytostatic; cardioactive; antagonists may have neuroprotective; general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or mathacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated opolynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat diagnostic or research purposes. The proteins may be used in the treatment of wounds and charcterial pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative discorders. The proteins may also be used in the treatment of wounds and ceptide AAB58849 are used in the course of the luvention for the identification and characterisation of the polynucleotide and protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numerous other
                                                                                              Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
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47.6%; Pred. No. 6.2e-48;
tive 49; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 RMRASNELALAELEEEGKPEGPANSSKTC 210
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                                                                                                                                                                                                                        Claim 11; Page 1027-1028; 1425pp; English.
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WPI; 2000-587514/55.
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                                 N-PSDB; AAF18072
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coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rabio. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence represents the human Rabio protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                  invention describes a novel human Rabio cDNA sequence. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                  Preparation of human gene coding sequence, its encoded polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 530.5; DB 21;
55.8%; Pred. No. 6.6e-48;
Live 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:17619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB95340 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 18; 23pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                            98CN-0121911
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Matches 96; Conservative
                                                                                                                                                                                                                             Gao J;
                                                                                                                                                                                                                                                                 WPI; 2000-400723/35.
                                                                                                                                                                                                                                                                                          N-PSDB; AAA40104
                                                                                                                                                                                  (UYFU-) UNIV
                                                                                                                                                                                                                             Tu 0,
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                                                                                                                                       28-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999;
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                                                                                            28-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
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      CN1249345-A.
                                                 05-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a mammalian RAB protein. RAB proteins constitute the largest family of small Grpases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression and many also be used to identify expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                       Buckler AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 530.5; DB 21; Length 200; Pred. No. 6.6e-48; 46; Mismatches 29; Indels 1;
                                          RAB protein; GTPase; GTP binding; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                       Rutter M,
                                                                                                                                                                                                                                                                                                                                                     Vega R,
Amino acid sequence of human RAB10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB09979 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the gene in a biological specimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 39; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                     McIntosh B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.8%;
Matches 96; Conservative 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Rab10; Yap/Rab family
                                                                                                                                                                                                                        13-MAR-2000; 2000WO-US06330
                                                                                                                                                                                                                                                                 99US-0126083
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                                                                                                                                                                                                                                                                                                          (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-647233/62.
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                                                                                                                                                                                                                                                                                                                                                     Allen M, Abel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 AA;
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                                                                                                                                  WO200058464-A2
                                                                                                                                                                                                                                                                 25-MAR-1999;
                                                                                        Homo sapiens
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Homo sapiens

AAB09979;

RESULT 9 AAB09979

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The present invention describes primer sets for synthesising 5602 [ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dT primer and an oilgouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprises a least 15 nucleotides; or (b) a combination of an oilgonucleotide comprises a sequence complementary to the compress and an oilgonucleotide comprises a 5'-end sequence and an oilgonucleotide comprises a 5'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oilgonucleotide which comprises a 3'-end sequence, where the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs and primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs represent human cDNA sequences; AAH13628 and AAH13633 represent human amino acid sequences; and AAH13632 to AAH13632 represent human anino acid sequences; and AAH13632 to AAH13632 represent continue and which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKQ-YDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
    Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNKADEEQKROVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer antigen protein sequence SEQ ID NO:1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.0%; Score 530.5; DB 22; Length
55.8%; Pred. No. 6.66-48;
Live 46; Mismatches 29; Indels
Isogai T, Nishikawa T, Hayashi K, Saito K, Y.
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                              Claim 8; SEQ ID 17619; 2537pp + CD ROM; English.
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nes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 AA;
                                                                                                                                                                                      full-length cDNAs
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat glassides such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 530.5; DB 2
55.8%; Pred. No. 7.5e-48;
iive 46; Mismatches 29
                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 2014-2015; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #7257.
                                                                                                                                                                                                                                                                                                          disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG07266 standard; Protein; 218
                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                     99US-0124270.
                                                                   08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.8%
Matches 96; Conservative
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                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                        WPI; 2000-587513/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 AA;
                                                                                                                                                     ROSEN C A.
                                                                                                                                                                                                                                        N-PSDB; AAF16196
WO200055174-A1.
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                                                                                                 12-MAR-1999;
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                                 21-SEP-2000
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                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers; and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasponstics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and continuous and sequences as ABG00010-ABG30377 represent novel human classequences are supplication, but was obtained in electronic format directly from WIPO at the sequence at this patent did not appear in the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.9%; Score 529.5; DB 22; Length 218; 55.8%; Pred. No. 9.6e-48; tive ·46; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 41733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 37625; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB71647 standard; Protein; 207 AA
                                                                                                                     Tang YT;
                          30-MAR-2001; 2001WO-US08631
                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AA;
                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                         N-PSDB; AAS71453
                                                                                                                                                                                                                           biodiversity
11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30311), expressed DNA sequences (ABLIG176-ABL30311), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, G-protein, 32705, 23224, 27423, 32700, 32712, lung disorder, congenital anomaly, pulmonary congestion, oedema; haemorrhage,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 41733; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human 27423 G-protein.
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tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG67154 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                        PWD,
                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P
                                                                                                                                                                                                                                  11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                        ij
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Matches 100; Conservative
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMRASN 186
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RMEANN 181
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(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL15750
                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions
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                                                                                                      27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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The present sequence represents a human G-protein. The specification describes 3705, 2324, 27423, 32700 or 32712 small G-proteins. The G-protein polypeptides and polynucleotides are useful as a target for diagnosis and treatment of G-protein mediated or related disorders, and for identifying agonists and antagonists for diagnosis and treatment. They are useful for treating disorders of lung (e.g. congenital anomalies, pulmonary congestion, oedema, adult respiratory distress syndrome, haemorrhage, chronic obstructive pulmonary disease, asthma, Goodpasture's syndrome and pulmonary hypertension), liver (e.g. hepatic injury, jaundice, cholestasis, viral hepatitis, cirrhosis, Wilson's disease, autoimmune hepatitis and hepatic failure), and corpus and siscered is chemical ischemia, intracranial haemorrhage, acute meningitis, Parkinson's disease, Alzheimer's disease, gliomas, chronic paterial meningencephalitis, multiple sclerosis, amyotropic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
adult respiratory distress syndrome; Goodpasture's syndrome; chronic obstructive pulmonary disease; asthma; pulmonary hypertension; liver disorder; hepatic injury; jaundice; cholestasis; viral hepatitis; cirrhosis; Wilson's disease; autoimmune hepatitis; hepatic failure; brain disorder; hypoxia; cerebral ischemia; intracranial haemorrhage; acute meningitis; Parkinson's disease, Alzheimer's disease; glioma; chronic bacterial meningencephalitis; multiple sclerosis; amyotropic lateral sclerosis; stroke; Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKES-FTRLTELVLOAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides for
brain disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
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54.0%; Pred. No. 1.1e-47;
tive 47; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human small G-protein polypeptides and
treating lung disorders, liver disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sclerosis, stroke and Huntington's disease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 15; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                   27-FEB-2001; 2001WO-US06292.
                                                                                                                                                                                                                                                                                                                                             29-FEB-2000; 2000US-0185606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 95; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-550182/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAG67154.
                                                                                                                                                                                                                       WO200164887-A2.
                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                              07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Meyers RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches
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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oilgo-dr primer and an oilgonucleotide comprises one of
the complementary strand of a polynucleotide which comprises one of
cligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oilgonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide comprises a 5'-end
complementary strand of a polynucleotide and the combination of
complementary strand of a polynucleotide and the combination of
complementary strand of a polynucleotides and the combination of
complementary strand of sequence is selected from those defined in
the 5'-end sequence 3'-end sequence is selected from those defined in
the 5'-end sequence 3'-end sequence is selected from those defined in
the principle comprises are also useful for the
complementary full-length cDNAs. The primers are also useful for the
complementary without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH13634 represent human cDNA sequences; and AAH13629 to AAH13632
crepresent oilgonucleotides, all of which are used in the exemplification
complementary invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
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                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                         Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                         Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 10930; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.1e
                 protein sequence SEQ ID NO:10930
                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T, Haya
Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                    99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                  99JP-0248036
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Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                 (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
                                                                                                                                                                                                                                                                                      11-JAN-2000;
02-MAY-2000;
                                                                                             Homo sapiens
                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                  29-JUL-1999;
                                                                                                                                                                                                                                                                        27 -AUG-1999;
                                                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Ota T, IS
Ishii S,
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Search completed: June 18, 2003, 15:33:30 Job time: 72 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 18, 2003, 15:30:31; search time 40 Seconds (without alignments) 509.512 Million cell updates/sec

US-09-817-198B-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Result		& Ouerv			SUMMARLES	
No.	Score	Match	Length	DB	a	Description
1	1077	97.5	212	7	F42148	GTP-binding protei
7	559	50.6	224	7	T33855	
m	545	49.3	207	~	B49647	_
4	545	49.3	207	~	B36364	
ß	532	48.1	203	~	A49647	
9	531.5	48.1	200	N	A38625	GTP-binding protei
7	530.5	48.0	200	~	D36364	GTP-binding protei
œ	530	48.0	209	~	B38625	GTP-binding protei
6	526	47.6	206	~	178851	
10	522.5	47.3	200	7	B42148	
11	519	47.0	216	7	T45901	\mathbf{a}
12	514	46.5	201	7	T28971	hypothetical prote
13	512	46.3	216	~	S33900	GTP-binding protei
14	512	46.3	216	~	T48378	
15	510	46.2	200	~	S12790	
16	509	46.1	215	~	T14565	
17	508.5	46.0	215	7	S57478	GTP-binding protei
18	208	46.0	216	~	JS0640	
19	507.5	45.9	222	~	T14405	small GTP-binding
50	206	45.8	216	~	S57471	GTP-binding protei
21	505.5	45.7	217	~	S36365	GTP-binding protei
22	502.5	45.5	215	~1	S57462	
23	501	45.3	203	7	S51495	
24	495.5	44.8	204	~	JC7589	Sec4p homolog - ye
25	492.5	44.6	215	~	S57474	5 to
56	483.5	43.8	208	~	A34716	
27	483	43.7	208	~	A38202	
28	482	43.6	. 203	~	S34253	
53	480	43.4	202	7	S38740	GTP-binding protei

RESULT 2
T33855
Hypothetical protein D1037.4 - Caenorhabditis elegans
Cypecies: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000
C;Accession: T33855
R;Ledwith, J; Blewald, T.
R;Ledwith, J; Blewald, T.
R;Description: The sequence of C. elegans cosmid D1037.

212

181 RMRASNELALAELEEEGKPEGPANSSKTCWC

g ò 요

30 479 43.3 203 2 B34716 31 477 5 43.2 2012 2 S72515 33 477.5 43.2 2012 2 S72515 34 477 43.2 2012 2 S72816 34 477 43.2 2012 2 S7105 36 476 43.1 258 2 B86153 37 475 43.0 203 2 JC24105 38 475 43.0 203 2 JC24105 39 473.5 42.9 205 2 T33781 40 473 42.8 206 2 T183781 41 473 42.8 206 2 T183781 42 470.5 42.6 2103 2 B38202 43 470.5 42.6 2103 2 B38202 44 469 42.4 205 1 TVRTYP 45 42.0 8 42.4 205 1 TVRTYP 46 42.4 205 1 TVRTYP 47 42.8 30.8991616 C) Date: 30.899-1993 #sequence_revision C) Caces: 30.899-1993 #sequence C) Caces: 30.899-199-199-199-199-199-199-199-199-199-	30 479 43.3 203 31 477.5 43.2 203 33 477.5 43.2 203 34 477.5 43.2 203 34 477.5 43.2 203 35 476 43.1 256 37 475.5 43.0 203 38 475.5 43.0 203 38 473.5 42.8 206 41 473.5 42.8 206 42 470.5 42.6 203 43 470.5 42.6 203 44 469 42.4 205 45 470.5 42.6 203 46 42.4 205 47 42.8 206 48 42.4 205 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 48 470.5 42.6 203 5000.0 Chem. 267, 576.5 576 500.0 Chem. 267, 576.5 576	479 473 478 473 478 473 473 473 474 43.2 477 43.2 476 43.1 477 43.2 476 43.1 473 42.8 473 42.8 473 42.8 473 42.8 473 42.8 473 42.8 42.4 468 42.6 42.6 42.6 42.6 42.6 42.6 42.6 42.6	13.3 13.3 13.2 13.2 13.2 13.2 13.2 13.2	479 43.3 203 2 B34.7 478 43.3 202 2 S722 478 43.3 202 2 S722 43.2 201 2 JC22 477 43.2 201 2 JC22 477 43.2 201 2 JC22 2 S72 477 43.2 201 2 JC22 2 S72 477 43.2 201 2 JC22 2 S72 43.0 202 2 JC22 43.0 203 2 JC23 473 42.8 206 2 T33 42.8 206 2 J5 J7 42.8 206 J7 42.8 207; CONSELVARIAL GDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 MAKQXDVLFRLLIGDSGVGKT 1 J7 J7 1 J7 1 J7 1 J7 1 J7 1 J7 1 J7	003 22 002 22 002 22 003 22 003 22 003 22 003 22 003 22 003 22 003 22 003 22 005 22 00	GNMENTS GNMENTS GNMENTS GNMENTS (t) 30-Sep-1993 R.H. elight GTP-bi 33; PMID:131 Elight GTP-bi 33; PMID:131 (Cys) (Cova (Cys) (### Carp-binding proteing GTP-binding GTP-bindin	protei pr	express logy logy systeine
Oy Dp	121	NKAD) NKAD)	EEOKR EEOKR	QVGRE(QVGRE([005 	NKADEBOKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 	SFTRLTELVLQAHRKELEC 		

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GTP-binding protein rab8 - dog

GTP-binding protein rab8 - dog

C; Species: Canis lipus familiaris (dog)

C; Species: Rais lipus familiaris (dog)

C; Species: Bar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001

C; Accession: B36364; S15604

Mol. Cell. Biol. 10, 6578-6585, 1990

A; Title: Molecular cloning of YPTI/SEC4 related cDNAs from an epithelial cell line.

A; Reference number: A36364; MUID:91061765; PMID:2123294

A; Reference number: A36364; MUID:91061765; PMID:2123294

A; Residues: Preliminary

A; Molecule type: MRNA

A; Residues: 1-207 < CHA>

A; CHA>

A; Coss-references: GB:X56385; NID:9920; PIDN:CAB56776.1; PID:96006436

C; Superfamily: ras transforming protein; translation elongation factor Tu homology

C; Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loo

F; 9-124/Region: translation elongation factor Tu homology < F; 15-72/Region: GTP-binding motif R (P-loop)

F; 15-124/Region: GTP-binding NKZD motif

F; 151-124/Region: GTP-binding SMXL motif

F; 204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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R;Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Lou Cell Biol. 124, 101-115, 1994
A;Title: A small rab Grase is distributed in cytoplasmic vesicles in non polarized c A;Reference number: A49647; MUID:94124602; PMID:8294494
A;Accession: A49647
A;Status: preliminary
A;Molecule type: mRNA
A;Esidus: p. 1-203 < 2AA>
A;Residus: 1-203 < 2AA>
A;Cross-references: EMBL:X75593; NID:9452319; PIDN:CAA53266.1; PID:9452320
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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                                                                                                                      NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                     61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IMDTAGQERFRITTTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.3%; Score 545; DB 2; 52.9%; Pred. No. 2.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9*
Matches 99; Conservative
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                                                                                                                                                                                                                                                            A;Map position: 1
A;Introns: 10/3; 62/2; 82/3; 181/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
                                                                                                                                            A;Cross-references: EMBL:AF106592; PIDN:AAC78494.1; GSPDB:GN00019; CESP:D1037.4
A;Experimental source: strain Bristol N2; clone D1037
C;Genetics:
A;Gene: CESP:D1037.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKTYDYLFKILLIGDSGVGKTCYLFRFSDDSFNNSFISTIGIDFKIRTIELDGKKIKLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: B49647
A;Actacis: nucleic acid sequence not shown
A;Actatus: nucleic acid sequence not shown
A;Residues: 1-207 <ZAH>
A;Residues: 1-207 <ZAH>
A;Cross-references: EMBL:X56741; NID:g452317; PIDN:CAA40065.1; PID:g452318
B;Joberty, G.; Tavitian, A.; Zahraoui, A.
FEBS Lett. 330, 323-328, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                               ; Score 559; DB 2;
; Pred. No. 2.1e-37;
42; Mismatches 39
                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                  tch 50.6%; al Similarity 55.3%; 105; Conservative 4
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A; Molecule type: mRNA
A; Residues: 175-186 <JOB>
                                                                                       A; Molecule type: DNA
A; Residues: 1-224 <LED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S36817
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Matches
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Tu homology binding; P-loo

29 9

Gaps

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C; Species: Discopyge ommate crecimic and version 23-Aug-1991 #text_change 02-Feb-2001 C; Species: Discopyge ommate crevision 23-Aug-1991 #text_change 02-Feb-2001 C; Accession: B38625 C; Accession: Baselinary C; Accession: 
            C; Accession: D36364; S15601
R; Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A; Title: Molecular cloning of YPT1/SE04 related cDNAs from an epithelial cell line. A; Reference number: A36364; MUID:91061765; PMID:2123294
A; Accession: D36364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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NKCDMNEKRQVSKERGEKLAIDYGIKF-ETSAKSSINVERAFITLARDIMTKLNKKM--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-200 (CHAS)
A;Cross-references: GB:X56387; NID:g914; PIDN:CAA39798.1; PID:g915
C;Superfamily: ras transforming protein; translation elongation factor Tu horizondes: GTP binding; lipoprotein; membrane trafficking; nucleotide bind F:10-125/Domain: translation elongation factor Tu homology (ETU)
F:16-23/Region: dTP-binding motif A (P-loop)
F:122-125/Region: GTP-binding NKXD motif F:152-154/Region: GTP-binding SaK/L motif F:152-154/Region: GTP-binding seranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 200;
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GTP-binding protein ora2 - electric ray (Discopyge ommata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Mismatches 29;
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47.4%; Pred. No. 3.9e-35;
ative 56; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 530.5; DB 2
Pred. No. 3.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%;
55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Conservative
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Best Local S
Matches 96,
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C) Species: Discopyge ommata
C) Species: Discopyge ommata
C; Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C; Accession: A38625
R; Mgsee, J. K.; Elferink, L.A.; Scheller, R.H.
J. Biol. Chem. 266, 2675-2680, 1991
A; Title: A family of ras-like GTP-binding proteins expressed in electromotor neurons.
A; Reference number: A38625; MUD:9115900; PMID:1899244
A; Accession: A38625
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-200 AnGS>
A; Cross-references: GB:M38390; NID:9213114; PIDN:AAA49230.1; PID:9213115
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Superfamily: ras transforming mortin; nucleotide binding; P-loop
F; 10-125/Domain: translation elongation factor Tu homology <br/>F; 10-125/Domain: translation elongation factor Tu homology <br/>F; 10-125/Region: GTP-binding MCXD motif<br/>F; 152-125/Region: GTP-binding NXXD motif<br/>F; 152-125/Region: GTP-binding NXXD motif
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F; 9-124/Domain: translation elongation factor Tu homology <ETU>
F; 15-22/Region: nucleotide-binding motif A (P-loop)
F; 121-124/Region: GTP-binding NKXD motif
F; 121-124/Region: GTP-binding SAK/L motif
F; 121, 22, 40, 121, 122, 124, 151/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #stc F; 200/Binding site: farnesyl (Cys) (covalent) #status predicted
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GTP-binding protein rabl0 - dog
C.Species: Canis lupus familiaris (dog)
C.Spate: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                                                                            48.1%; Score 532; DB 2;
47.6%; Pred. No. 2.6e-35;
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56.4%; Pred. No. 2.8e-35;
ive 44; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 GRRSGN-----GNKP--PSTDLKTC 192
                                                                                                                                                                                                                                                                                                                         49; Mismatches
                                                                                                                                                                                                                                                                                            Best Local Similarity 47.6 Matches 100; Conservative
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NiAlternate names: protein F4P12.310
NiAlternate names: protein F4P12.310
Sispecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04 Feb-2000 #sequence_revision 04 Feb-2000 #text_change 02-Sep-2000
C;Accession: T45901
C;Accession: T45901
Siblocker, H: Mewes, H:W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, Submitted to the Protein Sequence Database, January 2000
A;Reference number: 223016
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                                                                                                                                                                                                                                          61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA----HRKELE 178
                                                                                                                                64
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                                                                                                    1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T23H2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.0%; Score 519; DB 2; Length 216; 51.9%; Pred. No. 3e-34; Indels 42; Mismatches 43; Indels
                                               Indels
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R; Wammaley, P.; Bradshaw, H.
submitted to the EMBL Data Library, January 1997
A; Description: The sequence of C. elegans cosmid T23H2.
A; Reference number: Z20549
A; Recession: T28971
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                      Pred. No. 1.5e-34;
; Mismatches 30;
55.2%; Pic.
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-216 < CBLO>
A, Cross-references: EMBL:AL132966
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Best Local Similarity 51.9%;
                                            95; Conservative
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                   Similarity
                      Local
                      Best Loc
Matches
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: B42148
R;Elferink, L.A.; Anzai, K.; Scheller, R.H.
A;Elferink, L.A.; Anzai, K.; Scheller, R.H.
A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically expressed A;Reference number: A42148; MUID:92210533; PMID:1313420
A;Accession: B42148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: ras transforming protein; translation elongation factor Tu homology C; Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine F;9-124/Domain: translation elongation factor Tu homology <ETU> F;15-22/Region: nucleotide-binding motif A (P-loop) F;121-124/Region: GTP-binding NKXD motif F;151-153/Region: GTP-binding SAK/L motif F;203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Residues: 1-200 AELEP
A; Residues: 1-200 AELEP
A; Cross-references: GB:M83677
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine
F;10-125/Domain: translation elongation factor Tu homology E;10-23/Region: nucleotide-binding motif A (P-loop)
F;12-125/Region: GTP-binding NIXD motif
F;152-125/Region: GTP-binding SAK/L motif
F;199,200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                            GTP-binding protein MEL - mouse
N;Alternate names: gene MEL protein
C;Specias: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Feb-2001
C;Accession: 178851
R;Nimmo, E. R.; Sanders, P.G.; Padua, R.A.; Hughes, D.; Williamson, R.; Johnson, K.J.
Oncogene 6, 1347-1351, 1991
A;Title: The MEL gene: a new member of the RAB/TPT class of RAS-related genes.
A;Reference number: ISB355; MUID:91360267; PMID:1886711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.6%; Score 526; DB 2; 56.4%; Pred. No. 7.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: I78851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches
                                                                        ----NENSLQEAVDKLKSPPKKPSQKKK 200
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                     A; Cross-references: EMBL:U80033; PIDN:AAC48200.1; GSPDB:GN00019; CESP:T23H2.5
A; Experimental source: strain Bristol N2; clone T23H2
C;Genetics:
A;Gene: CESP:T23H2.5
A;Map position: 1
A;Introns: 43/1; 147/2; 173/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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GTP-binding protein ypt2 - tomato
GTP-binding protein ypt2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum
C;Species: Lycopersicon esculentum
C;Species: Lycopersicon esculentum
C;Species: Lycopersicon esculentum
R;Fleming, A.J.; Mandel, T.; Roth, I.; Kuhlemeler, C.
R;Reference number: S33899; MUID:9322691; PMID:8467223
A;Ttle: The patterns of gene expression in the tomato shoot apical meristem.
A;Reference number: S33899; MUID:9322691; PMID:8467223
A;Residues: 1-216 <FL2>
A;Residues: 1-216 <FL2>
A;Cross-references: GB:X69980; NID:9313028; PIDN:CAA49600.1; PID:9313029
C;Genetics:
A;Gene: Typt2
C;Superfamily: ras transforming protein; translation elongation factor Tu homolc C;Keywords: GTP binding; membrane protein; nucleotide binding motif A (P-loop)
F;128-131/Region: GTP-binding WKXD motif R;128-131/Region: GTP-binding SAK/L motif
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                                                                                                                                                                                                                              Query Match
46.5%; Score 514; DB 2; Length 201;
Best Local Similarity 46.9%; Pred. No. 7e-34;
Matches 100; Conservative 48; Mismatches 51; Indels 14;
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46.3%; Score 512; DB 2;
Best Local Similarity 50.5%; Pred. No. 1.1e-33;
Matches 99; Conservative 41; Mismatches 44
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189 EPQSIRINQSDQAGTA 204
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A; Residues: 1-201 <WAM>
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A,Title: Structural and functional analysis of ypt2, an essential ras-related gene in A,Reference number: S12790; MUID:90269232; PMID:2112089
                                                                                                                                                                                                                                         Mewes, H.W.; Rudd, S.; Lemcke,
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N'Alternate names: protein F12E4.300
C;Speciee: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: 148378
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, March 2000
A;Accession: 148378
A;Status: ....
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Sate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: S12790; S10493; T39214
R;Haubruck, H.; Engelke, U.; Mertins, P.; Gallwitz, D.
EMBO J. 9, 1957-1962, 1990
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A.Residues: 1-200 <FRAN>
A.Residues: 1-200 <FRAN>
A.Cross-references: EMBL:X52864; NID:95149; PIDN:CAA37045.1; PID:95150
A.Cross-references: EMBL:Data Library, September 1997
A.Reference number: 221836
A.Accession: T39214
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-200 <HAU>
A;Residues: 1-200 <HAU>
A;Cross-references: EMBL:X52469; NID:95143; PIDN:CAA36707.1; PID:95144
R;Fawell, E.; Hook, S.; Sweet, D.; Armstrong, J.
Nucleic Acids Res. 18, 4264, 1990
A;Title: Novel YPT1-related genes from Schizosaccharomyces pombe.
A;Reference number: S10492; MUID:90332438; PMID:2115995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
A; Map position: 5
A; Introns: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A; Note: F12E4.300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.3%; Score 512; DB 2; L
Best Local Similarity 49.8%; Pred. No. 1.1e-33;
Matches 100; Conservative 43; Mismatches 46;
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189 EPQGIKITKQDTAASSSTAEK 209
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-216 <BEV>
A;Cross-references: EMBL:AL162751
                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: DNA
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A; Residues: 1-200 <MCD>

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A;Gene: ypt2
A;Gene: ypt2
A;Gene: ypt2
A;Amp position: 1
A;Map position: 1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Superfamily: ras transforming membrane trafficking; nucleotide binding; P-loop;
C;Keywords: GTP binding: 1ipoprotein; membrane trafficking; nucleotide binding P-loop;
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;10-125/Region: nucleotide-binding next A (P-loop)
F;12-125/Region: GTP-binding NaXD motif
F;12-125/Region: GTP-binding SAK/L motif
F;199,200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
A;Cross-references: EMBL: 299262; PIDN:CAB16405.1; GSPDB:GN00066; SPDB:SPAC9E9.07c
A;Experimental source: strain 972h-; cosmid c9E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.2%; Score 510; DB 2; Length 200; Best Local Similarity 51.9%; Pred. No. 1.4e-33; Matches 97; Conservative 39; Mismatches 43; Indels
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Job time : 50 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 18, 2003, 15:24:36; Search time 22 Seconds (without alignments) 399.681 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-817-198B-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	RB15_RAT P35289 rattus norv	RAB8_HUMAN P24407 homo sapten	P22128	P51153	_DISOM P22127	P24409			P70550	P55258 1	P17609	Q39433	P28186	CA	_RAT	P41924	_picbi	_MAIZE P16976	P40392	P20791	015286	039571	001830	P28188							ST		FPT1 SCHPO P11620 schizosacch
	E E	RBJ	RAE			RAO1	RBJ	RBJ	RBB	RBE	RAE	YPI	RAE	AR	L YPI	RB1	RYL1	SAS	YPT1	RIC	SAS	RB3	r YPJ	I YP1	AR	L YPJ	L YPJ	SEC	I YPJ	SEC	L RB1	RAE	RB1	I YPJ
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dр	Query Match Length	97.5	49.3	48.8	48.1	48.1	48.0	48.0	47.8	47.8	47.6	46.2	46.1	46.0	45.7	45.5	45.4	43.8	43.7	43.4	43.3	43.2	43.2	43.2	43.1	43.0	43.0	42.8	42.6	42.6	42.4	42.4	42.4	42.3
	Score	1077	545	539.5	532	531.5	530.5	530.5	528.5	528.5	526	510	209	208	505.5	502.5	502	483.5	483	480	479	477.5	477.5	477	476	475.5	475	473	470.5	470.5	469	469	468	467
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36 456.5 41.3 206 1 YPT1_ENDOR 37 455.5 41.2 219 1 RB3C_RAT 38 454.5 41.0 190 1 RB2C_HUMAN 39 452.5 41.0 190 1 RB2C_HUMAN 45.5 40.7 220 1 RB3D_HUMAN 44.5 40.2 219 1 RB3D_HUMAN 42.5 40.0 219 1 RB3D_RNT 44.5 40.0 219 1 RB3D_RNT 44.5 40.0 219 1 RB3D_RNT 44.5 40.0 219 1 RB3D_RNT 44 44.1 39.9 220 1 RB3A_HUMAN 45 43 39.7 220 1 RB3A_HUMAN 45 439 39.7 200 1 RB3A_HUMAN 4	RB15_RAT STANDARD; PRT; P35289;	SULT 1 15_RAT	ALIGNMENTS	39.7 220 1 RB3A_HUMAN P20336	39.9 220 1 RB3A_MOUSE P05713	442.5 40.0 219 1 RB3D_RAT Q63942	444 40.2 219 1 RB3A_BOVIN P11023	444.5 40.2 219 1 RB3D_HUMAN 095716	449.5 40.7 220 1 RAB3_DROME P25228	452.5 41.0 190 1 RB26_RAT P51156	454.5 41.1 190 1 RB26_HUMAN Q9ulw5	455.5 41.2 219 1 RB3C_RAT Q63482	41.3 206 1 YPT1_YEAST P01123	FZELZ3	Solution 1 coc	asaccharomyc rattus norv homo saplen rattus norv drosophila homo saplen bos taurus rattus norv mus musculu homo saplen	P011123 Q03482 Q031186 P01186 P05218 P05318 P05318 P05313	N N N N N N N N N N N N N N N N N N N	TILTERSON 3C RAT 26 RAT 26 RAT 30 RAT 30 RAM 3D RAM 3D RAM 3D RAM ALIGNM ALIGNM	, , , ,	205 219 190 190 190 220 219 219 220 220 220 220	4444444444 0.111444444 0.121.000000000000000000000000000000000	4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 37 38 39 40 44 44 45 45 88 88 10 10 10 10 10 10 10 10 10 10 10 10 10
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                                                                                                                                                                                                                       NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                            61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-C.familiaris; STRAIN-Cocker spaniel;
MEDIINE-91061765; Pubmed-212394;
Charrier P., Vingron M., Sander C., Simons K., Zerial M.;
Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R., Tavitian A., Joberty G., Arpin M., Fontaine J.J., Hellio R.,
"A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1 in polarized epithelial cells.";
J. Cell Biol. 124:101-115(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606, 9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R., Johnson K.J.; "The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                  Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOI. Cell. Biol. 10:6578-6585(1990).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                  DB 1;
                Score 1077; DB 1;
Pred. No. 6.9e-80;
                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-UL-1998 (Rel. 36, Last annotation update)
Ras-related protein Rab-8 (Oncogene c-mel).
                                                                                                                                                                                                                                                                                                                                                                          RMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94124602; PubMed-8294494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91360267; PubMed-1886711;
                  97.5%;
97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens (Human), and
                                                             Matches 207; Conservative
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                                       Similarity
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P24407;
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                  Query Match
                                         Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IWDTAGOERFRITTAAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMIKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Buscopyge ommata (Electric ray).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; NCBL_TaxID=7785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GERECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
LEGNSPQ -> WKATAP (IN REF. 2).
WW. AASZDBF54A2CD056 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs; TIGR00231; small_GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 AA.
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TISSUE-Electric lobe;
MEDLINE-91115900; Pubmed-1899244;
Ngsee J.K., Elferink L.A., Scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR0013579; GTPase_Rab.
InterPro; IPR001209; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Ffan; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                      EMBL; X56741; CAA40065.1; -... EMBL; S53268; AAB19681.1; -... EMBL; B0002977; AAH02977.1; -... EMBL; X56385; CAB56776.1; -... PIR; B36334; B36364; B49647; B49
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67
124
45
204
183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC: 7007; MEL.
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177 1
207 AA;
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RAB8_DISOM
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RAO1_DISOM
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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"A family of ras-like GTP-binding proteins expressed in electromotor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R., Aravitian A., Louvard D.;
"A small rab GrPase is distributed in cytoplasmic vestcles in non polarized cells but colocalizes with the tight junction marker ZO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                         . Biol. Chem. 266:2675-2680(1991).
!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
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GERANYL-GERANYL (BY SIMILARITY).
OF73EDBODB8B9EEA CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RMRASNELALAE-LEEEGKPEGPANSSK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                         HASP: P05713; 3RAB.
InterPro; IPR0013579; GTPase_Rab.
InterPro; IPR001259; Prenyl_site.
InterPro; IPR0010805; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SW00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
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MEDLINE-94124602; PubMed-8294494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24164 MW;
                                                                                                                                                                                                                                                                                    EMBL; M38391; AAA49232.1; -. PIR; B38625; B38625.
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210 AA;
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Best Local Similarity
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P51153;
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NP_BIND
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RB13_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: COULD PARTICIPATE IN POLARIZED TRANSPORT, IN THE ASSEMBLY AND/OR THE ACTIVITY OF TIGHT UNCTIONS.
-i- SUBCELLUIAR LOCATION: CYPOPLASMIT TIGHT JUNCTIONS OR ASSOCIATED WITH VESICLES SCATFERD THROGGHOUT THE CYTOPLASM IN CELLS LACKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: VARIETY OF EPITHELIA, INCLUDING INTESTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                        KIDNEY, LIVER, AND OF ENDOTHELIAL CELLS.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prenylation; Protein transport.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
MW; 141621CB998178DA CRC64;
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                                                                                                                            Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Interpro; IPR001806; Ras_trosfrmng.
Interpro; IPR001806; Ras_trosfrmng.
Interpro; IPR00525; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SM00175; RAB; 1.
TIGRFAM9; TIGR00231; small_GTP; 1.
in polarized epithelial cells.";
J. Cell Biol. 124:101-115(1994).
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200 GE1
22774 MW;
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(Rel. 19, Last sequ
(Rel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC000799; AAH00799.1; -. HSSP; P01112; 1PLL. Genew; HGNC:9762; RAB13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X75593; CAA53266.1;
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                                                                                                                                                                                                                                                                                    TIGHT JUNCTIONS
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                                                                           SEQUENCE FROM N.A.
                                                                                                    TISSUE-Placenta;
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01-AUG-1991
01-AUG-1991
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P22127;
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Best Local S
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NP_BIND
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MEDLINE-91061765; PubMed-2123294;
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                                                                                                                                                                                                                                                                                                                                     38
199
200
200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RB10_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QIMDTAGQERFHTITTSYYRGAMGIMLYYDITNAKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                         SEQUENCE FROM N.A.
TISSUE-Electric lobe;
MEDLINE-91115900; Pubmed-1899244;
Migsee J.K., Elferink L.A., Scheller R.H.;
"A family of ras-like GTP-binding proteins expressed in electromotor
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Basmobranchi; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoidei; Narcinidae; Discopyge. NCBL_TAXID=7785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 531.5; DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
41D38E3D760519C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 4.9e-36; 44; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Ras-related protein Rab-10.
                                                                                                                               neurons.";
J. Biol. Chem. 266:2675-2680(1991).
-!- SIMILARITY: RAS-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                  HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                  SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
            Discopyge ommata (Electric ray).
                                                                                                                                                                                                                                                                                                                                                                                    23
68
63
125
22623 MW;
                                                                                                                                                                                                                                                               EMBL; M38390; AAA49230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Cocker spaniel;
                                                                                                                                                                                                                                                                         PIR; A38625; A38625.
                                                                                                                                                                                                                                                                                                                                                                                   16
64
122
200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                       GTP-binding
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P24409;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.; "Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERENYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
MW; 5D52B8E8E47D4362 CRC64;
                                                                                                                                                                               -! - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 200;
                                                                                      Mol. Cell. Biol. 10:6578-6585(1990).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding; Lipoprotein; Prenylation; Protein transport.
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Ras_related protein Rab-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003579; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00071; ras; 1.
PRINTS; PR0049; RASTRNSFRNG.
SMARI; SM0175; RAB; 1.
TIGREAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22569 MW;
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Best Local Similarity 55.88
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; D36364; D36364.
HSSP; P05713; 3RAB.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazawi Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ridota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Schriml L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baddarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D., Kamiya M., Lee N. H., Assanoto N., Kamiya M., Satok K., Schochbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K., Kawaji H., Kohtsuki S., M., Wang K., Wang K., Rawaji H., Kohtsuki S.,
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Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.; "Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning."; Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
                                                                                                                                                                                                                                                                                                               Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatama M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEUROTRANSMITTER RELEASE.
1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                        Wong K., Hong W., Tang B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Mouse;
Zeng O., Tan Y.H., Hong W.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Mouse; STRAIN-C57BL/6J; TISSUE-Stomach; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF106681; AAD43034.1; -. EMBL; AF297660; AAG13413.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Cervix;
                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                 SPECIES-Human;
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60 QIWDIAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"RAB GTPases expressed in human melanoma cells.";
Biochim. Biophys. Acta 1355:1-6(1997).
-!- FUNCTION: MAY BI THOULVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE (BY SIMILARITY).
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                     Protein transport.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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7F02B8E8E46EE1E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 530.5; DB 1; Pred. No. 5.9e-36; 46; Mismatches 29
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15-JUL-1999 (Rel. 38, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 AA
                                                                                                      MGD: MGI:105066; Rabio.
InterPro; IPR001879; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR001805; Small_GTP.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SM00175; RAB; 1.
TIGRRAMS; TIGR00231; Small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97182150; PubMed=9030196;
EMBL; AF035646; AAC29313.1; -. EMBL; AK0089725; BABZ5858.1; -. HSSP; P05713; 3RAB
Genew; HGNC:9759; RAB10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%;
55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ras-related protein Rab-8B.
RAB8B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AA;
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IWDTAGQERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96393028; PubMed-8799816; Armstrong J., Thompson N., Squire J.H., Smith J., Hayes B., Solari B. Identification of a novel member of the Rab8 family from the rat J. Cell Sci. 109:1265-1274(1996).

-!- PORCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE (BY SIMILARITY).

-!- TISSUE SPECIFICITY: HIGHEST LEVELS OF EXPRESSION IN THE SPLEEN, TESTIS AND BRAIN.
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                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

GERANYL.GERANYL (BY SIMILARITY).

5960993COFB7F944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 207;
                                                                                                                                       EMBL; AB038995; BAA92249.1; -.
EMBL; BC020654; AAH20654.1; -.
EMBL; UG6624; AAC51199.1; -.
HSSP; D65713; 3RAS.
InterPro; IPR0013579; GTPase_Rab.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001235; Small_GTP.
Pfam; PF00071; ras; 1.
Pfam; PF00071; ras; 1.
SMART; SM00175; RAB; 1.
IIGREAM; TGR00231; small_GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.8%; Score 528.5; DB 1; Length 54.0%; Pred. No. 8.9e-36; Live 47; Mismatches 33; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Ras-related protein Rab-8B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                204 GE
23584 MW;
                                                                                                                                                                                                                                                                                                                                                           GTP-binding; Prenylation; 18 22 18 NP_BIND 63 67 NP_BIND 121 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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37
204 2
207 AA;
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P70550;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removéd. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R., Johnson K.J.; "The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Öncogene 6:1347-1351(1991).
-!- FUNCTION: MAY BE INVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 207;
                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EPFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

4441AB26BF9DCAF4 CRC64;
                                                                                                                                               InterPro; IRRO13579; GrPase_Rab.
InterPro; IRRO1310; Prenyl_site.
InterPro; IRRO1806; Ras_trnsfrmng.
InterPro; IRRO1806; Ras_trnsfrmng.
InterPro; IRRO1806; Ras_trnsfrmng.
PRINTS; PRO0471; ras; 1.
PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM0175; RAB; 1.
TIGRFAMS; TCGR0231; small_GFP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%; Score 528.5; DB 1
54.0%; Pred. No. 8.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
RAB8 OR MEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.0%; Preq. ...
"*** Local Similarity 54.0%; Mismatches
"*** Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-91360267; Pubmed-1886711;
                                                                                                                                                                                                                                                                                                                                                                                                23603 MW;
                                                                                                                    EMBL; U53475; AAA99782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                            204 2
207 AA;
                                                                                                                                      P05713;
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                        61 IWDJAGQERFRIITAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
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                                                                                                                                                                                                                                                                 MEDLINE-90269232; PubMed-2112089;
Hengst L., Lehmeier T., Gallwitz D.;
"Structural and functional analysis of ypt2, an essential ras-related
gene in the fission yeast Schizosaccharomyces pombe encoding a Sec4
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-21848401; PubMed-11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
                                                                                                                                                                                                                                   ö
                                                                                                                                        GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GFF (BY SIMILARITY).

GFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

49D832725D662942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-90332438; PubMed-2115995;
Fawell E., Hook S., Sweet D., Armstrong J.;
"Novel YPFI-related genes from Schizosaccharomyces pombe.";
                                                                                                                                                                                                             47.6%; Score 526; DB 1; Length 206; 56.4%; Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                               121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                 SWART; SM00175; RAB; 1.
TIGREAMs; TIGR00231; small_GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                  31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2014 protein ypt2.
                                                                                                                                                                                                                                                                                                                                                                                                        200 AA
                                                                                                                                                                                                                                 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:4264-4264(1990)
                                                InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                             MGD; MGI:96960; Mel.
InterPro; IPR003579; GTPase_Rab.
                                                                             Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                           23557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein homologue.";
EMBO J. 9:1957-1962(1990).
         EMBL; S53270; AAB19682.1;
                                                                                                                                                                                                                                 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                          22
67
124
45
203
                                                                                                                                                                                           206 AA;
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                                                                                                                             Proto-concogene.
NP_BIND 15
NP_BIND 63
NP_BIND 121
DOMAIN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                      YPT2_SCHPO
P17609;
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                                                                                                                                                                                                               Query Match
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Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidatel T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidatel T., Fraser A.,
RA Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Ammes K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Monory P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,
A. O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Saunders D., Seeger K., Sharp S.,
Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Paylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Paylor K., Taylor R.G., Aert R., Robben J., Grymonprez B.,
ROCOWARD J., Volckaert G., Aert R., Robben J., Grymonprez B.,
ROCOWARD J., Vanstreels E., Rieger M., Schaefer W., Wheller H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
R Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
R Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
R Cerrutti L., Lowe T., McCombie W.R., Paulsen I.,
R Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
R The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KOYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIOIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAFFIC (BY SIMILARITY).
-1- MISCELLANBOUS: THIS PROTEIN IS ESSENTIAL FOR CELL VIABILITY.
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
PROBABLE YEAST SEC4 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 415:871-880(2002).
-!- FUNCTION: PROTEIN TRANSPORT, PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
GERANYL.GERANYL (BY SIMILARITY).
GERANYL.GERANYL (BY SIMILARITY).
W; 2C658D153A29OC30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein; Prenylation; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%; Score 510; DB 1;
51.9%; Pred. No. 2.6e-34;
iive 39; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_Grp.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             small_GTP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003579; GTPase_Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SMO0175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22755 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52469; CAA36707.1; -. EMBL; X52864; CAA37045.1; -. EMBL; Z99262; CAB16405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.9%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S10493; S10493.
PIR; S12790; S12790.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIE_AN
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184 ASNELALAELEEEGKPEGPANSSKTCWC 212
                                       190 AQPSITIKPADQ-----SGNQAAAKSACC 213
                                                                                                    ARA3_ARATH
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          AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFRMKTIEVDGIKVRIQIMDT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. DIOG KS 38080;
MEDLINE-96307523; PubMed-8680960;
Mallery E., Quief S., Ben Jilany K.E., Kerckaert J.-P., Hagege D.;
Molecular cloning and structural analysis of cDNAs that encode 3 small GTP-binding proteins from sugar beet.",
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GERANYL-GERANYI. (BY SIMILARITY).
GERANYL-GERANYI. (BY SIMILARITY).
M, 781CCSA17F29BBAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
6
46.1%; Score 509; DB 1; Length 215; 47.8%; Pred. No. 3.5e-34; 1ve 42; Mismatches 59; Indels
                                                                                                                                                                    (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP-binding; Lipoprotein; Prenylation. NP_BIND 22 29 GTP (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IRR003579; GTPBASE_RAD.
InterPro; IPR001806; RAS_trnsfrmng.
InterPro; IRR005225; Small_GTP.
FRam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SWART; SM00175; RAB; 1.
TIGRFANS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49152; CAA89021.1; -. HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23787 MW;
                                                                                                                                                                                15-JUL-1998 (Rel. 36, Last
15-JUL-1998 (Rel. 36, Last
Ras-related protein RABIBV.
                                                                                                                                                                                                                                        Beta vulgaris (Sugar beet)
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                       183 RASNELA 189
                                                                   176 DAENEFS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                    15-JUL-1998
                                                                                                                                          RAB1_BETVU
Q39433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sim.
Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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NP_BIND
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                                                                                                                          RAB1_BETVU
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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Delsanoubat M., Grivell L.A., Mache R., Pujdomenech P.,
Babeny M., Boutry M., Grivell L.A., Mache R., Pujdomenech P.,
RA De Simone V. Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Murmbach E., Drzonek H., Erfie H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Woss H., Holland R., Brandt P., Nyakatura G.,
RA Conrad A., Hornischer K., Rauer G., Loehnert T.-H., Nordsiek G.,
RA Rochet J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Manhaupt G., Raase D., Schoof H., Rudd S., Zaccarla P., Mewes H.-W.,
RA Manhaupt G., Raase D., Schoof H., Rudd S., Zaccarla P., Mewes H.-W.,
RA Manhaupt G., Raase D., Schoof H., Rodd S., Zaccarla P., Mewes H.-W.,
RA Rooney T., Rizzo M., Walti R., Wu D., Peterson J., Van Aken S.,
Creasy T.H., Raas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Raser C.M., Kaneko T., Naelmaura Y., Salos T.P.,
RA Raser C.M., Kaneko T., Naemaura Y., Sato S., Rato T., Asamizu E.,
RA Riyokawa C., Kohara M., Matsumot M., Matsuno A., Muraki A.,
RA Rasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Rasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Ra Rasamoto S., Makazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda S., Chente Landa R., Rabathana.",
RA Watanabe A., Yamada M., Yasuda S., Itakawa S., Nakazaki N., Yasuda S., Itakawa S., Nakazaki N., Yasuda S., Itakawa S., Nakazaki N., Yasuda S., Itakawa S., Nakazaki S., Takakauchi C., Wada T.,
RA Kanabe A., Yamada A., Yanada A., Yanada A., Yanada S., Itakawa S., Itakawa S., Nakasaki S., Takakauchi C., Wada T.,
Ratanabe A., Yamada S., China S., Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities requires a license agreement is not removed. Usage by and for commercial or send an email to licenseelsb-sib.ch).
                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and analysis of cDNAs encoding small GTP-binding proteins of Arabidopsis thaliana.";
Gene 108:259-264(1991).
                                                                                                                                                                                                                                                                                                                                                                                         Anai T., Hasegawa K., Watanabe Y., Uchimiya H., Ishizaki R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:820-822(2000).
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                     (Rel. 24, Last sequence update)
(Rel. 41, Last annotation update)
       216 AA
                                                                                                                                                                                                                                                                                                                                          STRAIN=Various strains; TISSUE=Leaf;
MEDLINE=92084144; PubMed=1748311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016720; PubMed-11130713;
                                                                                                               Ras-related protein ARA-3.
ARA-3 OR AT3G46060 OR F12M12_30.
                                                 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL355775; CAB90933.1;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D01025; BAA00830.1;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                   01-DEC-1992
15-JUN-2002
                                           01-DEC-1992
ARA3_ARATH
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HSSP; P05713; 3RAB.
InterPro; IPR0013579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
InterPro; IPR003575; Small_GTPase.
                                                                                                         RASTRNSFRMNG.
                                                                                                                                                                                                                                                      24143 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ras-related protein Rab-10.
             EMBL; L08128; AAA34251.1;
PIR; S36365; S36365.
                                                                                                                                                                                                                                                                                                      Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                 27
72
129
50
215
216
                                                                                              Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTR
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                      217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                  Multigene family NP_BIND 68 NP_BIND 126 DOMAIN 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RB10_RAT
P35281;
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RB10_RAT
  셤
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                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                         72 AGQERFRITTAXYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                         125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                            AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                         12 YDYLIKLLIGDSGVGKSCILLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                                                                             5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fabry S., Jacobsen A., Huber H., Palme K., Schmitt R., astructure, expression, and phylogenetic relationships of a family of
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Genet. 24:229-240(1993).
-1- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAFFIC (BY SIMILARITY).
                                                                                                                                                                EFFECTOR REGION (BY SIMILARITY).
GERANYL.-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
09E9C19A7A44E705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ypt genes encoding small G-proteins in the green alga Volvox carteri.";
                                                                                                                                                                                                                             46.0%; Score 508; DB 1; Length 216; 46.9%; Pred. No. 4.2e-34;
                                                                                                                                                                                                                                                     54; Indels
                                                                                                                    Multigene family
                                                                                                                   GTP-binding; Lipoprotein; Prenylation; Multigene NP_BIND 22 29 GTP (BY SINILARITY) NP_BIND 770 74 GTP (BY SIMILARITY) NP_BIND 128 131 GTP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                           184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GTP-binding protein yptV2.
                                                                                                                                                                                                                                                      41; Mismatches
                                Interpro; IPR003579; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR001805, Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-f. Nagariensis / HK10;
MEDLINE-94037148; PubMed-8221932;
                                                                                                                                                                                                      23835 MW;
                                                                                                                                                                                                                                        Best_Local Similarity 46.9
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                 29
74
131
52
213
214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Volvocaceae; Volvox.
                       HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPT2_VOLCA
                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                      SEQUENCE
                                                                                                                             NP_BIND
NP_BIND
NP_BIND
DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGYQKILIGNKAD 124
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MEDILNE-9221033; PubMed-1313420;
Elferink L.A., Anzal K., Scheller R.H.;
"Rabl5, a novel low molecular weight GTP-binding protein specifically expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                             GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
GERANYL.GERANYL (BY SIMILARITY).
GERANYL.GERANYL (BY SIMILARITY).
W; 87D3B30C75689EAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 217;
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-1- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND
NEUROTRANSMITTER RELEASE.
SMART; SM00175; RAB; 1.
SMART; SM0010; small_GTPase; 1.
STGRFAMS; TIGRO0231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%; Score 505.5; DB 1; 48.6%; Pred. No. 6.7e-34;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 ASNELALAE-LEEEEGKPEGPANSSKTC 210
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKO-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
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R InterPro; IPR001806; Ras_trnsfrung.
R InterPro; IPR001806; Ras_trnsfrung.
R InterPro; IPR001255; Small_GTP.
R PEAM; PF00071; ras; 1.
R PRINTS; PR00449; RASTRNSFRMG.
R SMART; SM00175; RAB; 1.
R TGRFAMS; TGR00211; raal]_GTP; 1.
R GTP-binding; Lipoprotein; Prenylation; Protein transport.
R GTP-binding; Lipoprotein; Prenylation; Protein transport.
R P_BIND 16 23 GTP (BY SIMILARITY).
R P_BIND 122 125 GTP (BY SIMILARITY).
R DOMAIN 38 46 EFFECTOR REGION (BY SIMILARITY).
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46 EFF
199 GE
200 GE
22858 MW;
                                                                     ЕМВL; М83677; ААА41991.1; -.
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Best Local Similarity 53.58
Matches 92; Conservative
                                                                                          IR; B42148; B42148.
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38
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200 AA;
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Search completed: June 18, 2003, 15:34:00 Job time: 23 secs

us-09-817-198b-2.rspt

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0-1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 19.4 kDa protein.
Hypothetical 19.4 kDa protein.
By mas musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013790, AAH13790.1;
InterPro. IPR001806; Ras_trnsfrmng.
InterPro: IPR002078; Sig54_interact.
InterPro: IPR002078; Small_GTP.
R Fidm, PF00071; Tas; 1.
R TIGRFAMS; TIGR0231; Small_GTP:
R PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
M GTP-binding; Hypothetical protein.
SEQUENCE 168 AA; 19399 MW; 4E2C2FBIC56BCDF8 CRC64;
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; Pred. No. 3.7e-59;
1; Mismatches 0;
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Q95WW8
Q96GT4
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Q8M3J2
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Q6554
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Q08155
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Q92RE2
Q9D1G1
Q9UAQ6
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Q96362
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Q9SF91
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Best Local Similarity 99.39
Matches 152, Conservative
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SEQUENCE FROM N.A.
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09tys2 caenorhabdi
015971 drosophila
08vcf6 mus musculu
018338 drosophila
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09dd03 mus musculu
09dd03 mus musculu
02het4 aspergillus
040218 lotus japon
040215 lotus japon
09fjf1 arabidopsis
094148 caenorhabdi
040219 lotus japon
08wf9 nicottana t
040177 lycopersico
                                                                                              ; Search time 81 Seconds
(without alignments)
539.284 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Q9TYS2
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Q8VCF6
O18338
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Q9HET4
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Q40218
Q40215
Q9FJF1
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Q8VWF9
Q40177
                                                                                                June 18, 2003, 15:25:06
                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_fung1:*
sp_human:*
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sp_mhc:*
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Maximum DB
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        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoldea,
Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 211;
                                                                                                                                                                            -JUN-2002 (TrEMBLrel. 21, Last sequence update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
elegans RAB-8 protein (corresponding sequence D1037.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF106592; AAK21367.2; --
SEQUENCE 211 AA; 24022 MW; B7609A91B6082DA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid D1037.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015971 PRELIMINARY; PRT; 204 AA. 015971; 01-571; 01-571; 01-571-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) RABIO protein (LD39986P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.4%; Score 557; DB 5; 55.0%; Pred. No. 6.9e-39;
211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created) 01-JUN-2002 (TrEMBLrel. 21, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
Ledwith J., Biewald T.;
                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RMRASNELA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 EMRAGGSVS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.;
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                                                                                                               09TYS2
09TYS2;
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                                                                               RESULT 2
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                                                                                                   09TYS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                               GNKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IMDIAGOERERIITATYRGAMGIMLVYDITNEKSEDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                    1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                     1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                    49.5%; Score 546.5; DB 5; Length 204;
49.8%; Pred. No. 5e-38;
ive 47; Mismatches 50; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
Similar to mel transforming oncogene (derived from cell line
NKI4) RABB homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0294; PRENYLATION; UNKNOWN 1.
PROSITE; PSO0675; SIGMAS4_INTERACT_1; UNKNOWN 1.
SEQUENCE 207 AA; 23668 MW; AC89DC85588FB8FB CRC64;
                                                                               23336 MW; 4E058761C6854920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LRMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 RESAENQERVIIDRRNQEKAP----GYSKCC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA.
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InterPro; IPR002078; Sig54_interact.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC019990; AMI19990.1; -
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20,
                                                           Lipoprotein.
                                                                                                                                                                                               Conservative
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           PROSITE; PSUVO, C., GTP-binding; Lipopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                  Local Similarity
les 105; Conserv
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                                                                                                                                          Query Match
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                                                                                                                                                                        Best Loc
Matches
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Q8VCF6
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Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Satoh A.K., Tokunaga F., Ozaki K.;
"Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                               207 AA
                                                                                                                                                                                                               PRT;
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STRAIN-OREGON R; TISSUE-HEAD;
MEDLINE-97228579; Pubmed-9074639;
: |: :|: 181 SPQGSSHGVKITVEQQK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein family.";
FEBS Lett. 404:65-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                         RAB8 protein (LD44762p).
RAB8 OR CG8287.
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                        RESULT
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InterPro; IPR003579;
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                                                                                                                                                                                                                                                                                                                                       NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                   9
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
A. Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMB./ADBJ databases.
- I- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
REMBL, AR60351; AAF49101.1; -.
REMBL, AR60551; AAA1711.1; -.
REMBL, AR065671; AAA17916.1; -.
REMBL, AR065671; AAA17916.1; -.
REMBL, REMOUSTOS GTPASE RAB.
RICEPPO: IPRO01230; Prenyl_site.
RICEPPO: IPRO01230; Prenyl_site.
RICEPPO: IPRO01230; Ras_trnsfrmmg.
RICEPPO: IPRO01230; Sas_trnsfrmmg.
RICEPPO: IPRO02205; Small_GTP.
RICEPPO: IPRO02205; Small_GTP.
RICEPPO: IPRO02205; Small_GTP.
                                                                                                                                                                                                                                                                         1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                           47.8%; Score 528.5; DB 5; Length 207; 53.8%; Pred. No. 1.6e-36; Ive 41; Mismatches 40; Indels 5
                                                                                                                                                                                                          23691 MW; BE9DE812C77DCF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 22.5 kDa protein.
                                                                                                                                                PRINTS; PRO0449; RASTRNSFRANG.
SMART; SW00175; RAB; 1.
TIGRPAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00244; PRENYLATTON; UNKNOWN_1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AA
                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8%
Matches 100; Conservative
                                                                                                                                                                                                GTP-binding; Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          RMRASN 186
                                                                                                                                                                                                                                                                                                                                                                                     || |:|
RMEANN 181
                                                                                                                                                                                                         207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                          181
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Q9H0T3
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RAWAI J., SALDAGAWA A., Shibate K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibate K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibate K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Pukunishi Y., Konoo H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RAGOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAGOTA K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

RAGOTA K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RASAI K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rawstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Ray Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.

Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

Rordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shamata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Willming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ruture 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0610007N03R1K, Protein (RIKEN CDNA 0610007N03 gene).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GNKCDMDDKRVVPKGKGGQIAREHGIRFFETSAKANINIEKAFLTLAEDILR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AK002303; BAB22000 1; -
EMBL; BC027214; AAH27214.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                     TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMAS4_INTERACT_1; UNKNOWN_1.
GTP-binding; Hypothetical protein; Lipoprotein.
SEQUENCE 200 AA; 22469 MW; 7F01DB88E46EE3EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                       47.6%; Score 526.5; DB 4 55.8%; Pred. No. 2.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Mismatches
                             InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
GTPase_Rab
                                                                                                                                                                  PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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STRAIN-N402;

Punt P.J., Selboth B., Weenink X.O., van Zeijl C.M., Lenders M.,

Rontschnyf C., Ram A.F., Montijn R., Kubicek C.P.,

A Konteschny C., Ram A.F., Montijn R., Kubicek C.P.,

A Tolentification and characterisation of a family of secretion related and Idpress encoding genes from the filamentous fungus Aspergillus in injer: a putative SEC4 homologue is not essential for growth.";

C. I. SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.

REMBL, ALJ786589; CAC17832.1;

RESP: P05713; 3RAB.

InterPro; IPR0013579; GTPase_Rab.

InterPro; IPR001605; Rai_trnsfrmng.

InterPro; IPR005255; Small_GTP.

PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                    61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                  121 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVL 170
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                                                                                                                                                                                         Length 202;
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                                                                                                                                                                                      / Match 47.6%; Score 526; DB 11; Length 2 Local Similarity 54.1%; Pred. No. 2.5e-36; es 92; Conservative 45; Mismatches 33; Indels
                                                                                        PRINTS, PRO0449, RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; SMAll_GTP; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 202 AA; 22770 MW; 5DF599432E228AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP-binding; Lipoprotein.
SEQUENCE 206 AA; 22823 MW; 501916B795CF8CBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.1%; Score 521; DB 3; I
60.6%; Pred. No. 6.8e-36;
ive 30; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                  206 AA
        MGD; MGI:1915578; 0610007N03Rik.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Si954_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secretion related GTPase, (SrgA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5061;
                                                                                                                                                                                        Query Match
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Q9HET4
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                                                                                                 DIAGOERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
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     62
                                                   64
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Salanoubat M.;
ATRAB8 (GTPase ATRAB8).

RAB8 OR E4P12_310.

Arabidopsis thaliana (Mouse-ear cress).

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIOIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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9
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Bischoff F., Palme K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR0231; small_GTP; 1.
PROSITE; PS00675; SMAS4_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 216 AA; 23939 MW; 1648E45B29D4EEB6 CRC64;
                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                 123 ADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 519; DB 10;
Pred. No. 1.1e-35;
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                                                                                                                                                                                                                                                                                                                                                                             216
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1954_interact.
InterPro; IPR005225; Small_GTP.
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U82434; AAB65088.1; -.
EMBL; AL132966; CAB67668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Matches 100; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
japonicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPFJF1;
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MEDLINE-97231679; PubMed-9076991;

MEDLINE-97231679; PubMed-9076991;

MEDLINE-97231679; PubMed-9076991;

T "Identification of new protein species among 33 different small GTP-
"Identification of new protein species among 33 different small GTP-
"Identification of new protein species among 33 different small GTP-
"Identification of new protein species among 33 different small GTP-
"Identification of new protein species among 33 different small GTP-
"Identification of new protein species among 33 different small GTP-
"Intentification of new protein species among 33 different small GTP-
"InterPro: IPR001806; Ras_trnsfrmng."

InterPro: IPR001806; Ras_trnsfrmng.

InterPro: IPR001806; Small_GTP-
"InterPro: IPR001806; Small_GTP-
"InterPro: IPR00171; ras; InterPro: IPR00171; ras; IPR00171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceáe, Papilionoideae, Loteae, Lotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23627 MW; 5E1A6E83505E50D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                  Last sequence update)
Last annotation update)
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PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 518; DB 10;
48.6%; Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLRMRASNELALAELEEEEGKPEGPANSSKTC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches
                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Lipoprotein.
214 AA; 23627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel. (TremBLrel. )
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                                                                                                                              PRELIMINARY;
                                                                                                                                                               01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                        ::: |::
192 TIKINQSDQ 200
 179 GLRMRASNE 187
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-ROOT NODULES;
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                                                                                                                                                                                                                                                         Lotus japonicus
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040215;
01-NOV-1996 (
01-NOV-1996 (
01-JUN-2002 (
RABBA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MD-2002 (TrEMBLrel. 21, Last annotation update)
8ab-type small GTP-binding protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae, Lotus.
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"Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen
physically assigned P1 and TAC clones.";
DNA Res. 5:297-308(1998).
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Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima
                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-binding; Lipoprotein.
SEQUENCE 216 Aa; 23776 MW; 569926CCA8D1B489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.7%; Score 515.5; DB 1
48.3%; Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 ASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 A--EPQTIQINOPDASASGGQAAQKSC 213
                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003579; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrung.
Interpro; IPR002078; S1954_interact.
Interpro; IPR005225; Small_GTP.
PRINTS; PR000449; Ras_TRNSFRMNG.
SMART; SM00175; RAB; 1.
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22712 MW; 2D205ABF751EBF1A CRC64;

201 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                        72 AGQERERITTAYYRGAMGILLYYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                          125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                      132 MDESKRAVPKSKGQALADEYGIKFFETSAKTNLAVEEVFFSIAKDIKQRLADTDSRAEPA 191
                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                         12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT
                                                                                                                                                                                                                           5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIOIWDT
                                                                                                                                                                                                      Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonet M.L., Staunton J.E., Kilgard M.P., Fergestad T., Jorgensen Hartweig E., Horvitz H.R., Meyer B.J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                     16;
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AB015475; BAB08351.1; -.
HSSP; P05713; 3RAB.
                                                                                                                                                                             Length 216;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
Wamsley P., Bradshaw H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                       216 AA; 23834 MW; E1370672F6EF3364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                InterPro; IPR001879; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR002078; Sig54_interact.
Pfam; Pr00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNG.
SMART; SM00175; RAB; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
                                                                                                                                                                            46.6%; Score 515; DB 10; 147.6%; Pred. No. 2.3e-35; Live 43; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                         179 GLRMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                              192 TIKISQTDQAAGA-----GQATQKSAC 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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TIGRFAMS; TIGR00231; small_GTP; 1.
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(TrEMBLrel. 05, I
(TrEMBLrel. 21, I
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                                                                                                                                                                                         Local Similarity 47.6 les 101; Conservative
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01-JUN-2002
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                                                                                                                                                       SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
TISSUE-ROOT NODDLES;
MEDLINE-$7231679; PubMed-9076991;
BOTS S., Brandstrup B., Jensen T.J., Poulsen C.;
"Identification of new protein species among 33 different small GTP-binding proteins encoded by cDNAs from Lotos japonicus, and expression of corresponding mRNAs in developing root nodules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLOIMDT
                                                                                                                      Lotus japonicus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                             1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
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; Pred. No. 3.1e-35;
43; Mismatches 53; Indels 17; Gaps
                                                    Gaps
                                                  14;
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-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; Z73948; CAA98176.1; -.
HSSP; P05713; 3RAB.
Length 201;
                                               51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0675; SIGMAS4_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 215 AA; 23715 MW; E7912846E919D608 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
; Score 514; DB 5;
; Pred. No. 2.5e-35;
48; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                   172 AKMPDSTD----EQSRDTVNPVQPQRQSSGGC 200
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
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TIGREAMS; TIGR00231; SMA11_GTP; 1.
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PRINTS; PR00449; RASTRNSFRANG.
46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.5%;
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Matches 100; Conservative
                                               Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=34305;
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  Query Match
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65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRIGHT YELLOW 2;
TOTIMOTO N., Shimada K., Ito K., Yamamoto K.;
Torimoto N., Shimada K., Ito K., Yamamoto K.;
Torimoto N., Shimada K., Ito K., Yamamoto K.;
Torimoto N., Shimada K., Ito K., Yamamoto K.;
Characterization of Rab8 from tabacco BY-2 cell.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB079021; BAB84325.1;
Inter. AB079021; BAB84325.1;
Inter. Proc. IPR001806; Ras_trnsfrmng.
InterPro; IPR001806; Ras_trnsfrmng.
                                                                                                                                                                                   08VWF9;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ras-related protein RAB8-4 (Ras-related protein RAB8-2).
RAB8-4 OR RAB8-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWART; SWO0175; RAB; 1.
PROSITE; PSO0675; SIGMA54_INTERACT_1; UNKNOWN_1.
SEQUENCE 216 AA; 23971 MW; D5E87FABDOD49E13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

46.4%; Score 513; DB 10;

Best Local Similarity 46.7%; Pred. No. 3.4e-35;

Matches 99; Conservative 44; Mismatches 53;
                                                          178 EGLRMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                 179 GLRMRASNELALAELEEEGKPEGPANSSKTC 210
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                                                                                                                                                                          PRT;
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PRINTS; PR00449; RASTRNSFRANG
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4097;
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Search completed: June 18, 2003, 15:35:30 Job time : 83 secs

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1105
'I MAKQYDVLFRLLLIGDSGVG......LEBEBGRPEGPANSSKTCWC
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-531-525-25
US-08-531-525-51
US-08-531-525-51
US-08-531-525-35
US-08-531-525-10
US-08-531-525-10
US-08-718-270A-10
US-08-718-270A-10
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US-08-718-270A-10
US-08-718-270A-34
US-08-916-901-3
US-08-916-901-8
US-08-915-602-3
US-08-916-901-8
US-08-915-503-14
US-08-915-503-14
US-08-915-503-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-718-270A-13
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                                                                                                                                                                                                                                                                                                            262574 seqs; 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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409.5 37.1 409.5 409.5 409.5 37.1 409.5 37.1 409.5 37.1 409.5 37.1 409.5 37.1 409.5 37.1 409.5 37.1 200.5 37.1 200.5 37.1 200.5 37.1 200.5 37.1 200.5 37.1 200.5 37.1 200.5 37.1 35.0 33.0 33.0 33.0 33.0 33.0 33.0 33.0	2 US-08-718-270A-26 Sequence 26, ALIGNMENTS	US/08824873 US/08824873 Jennifer L. Rari NOVEL RAB PROTEIN SS: Pharmaceuticals, Inc. er Drive box Windows Version 2.0 ATA: costolory in US/08/824,873 di Herewith sis in US/08/824,873 fr: MATION: MATION: RATION: RATION: AND SS: AN
	32.5	3-4 NFCRAATION: NFCRAATION: NFCRAATION: NFT Guegler, F INVENTION: OF SEQUENCES: SSEE: Incyte T: 8174 Porte Palo Alto SSEE: Incyte T: 8174 Porte TES: 100 Por

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Gaps

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49.3%; Score 545; DB 2; Length 207; 52.9%; Pred. No. 2.2e-52; Ive 45; Mismatches 43; Indels

Query Match
Best Local Similarity 52.9
Matches 99; Conservative

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62 DTAGQERFRITTTAYY-RAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILGNK 120
                                         NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                             63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
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61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                             APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Poncus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Kande, Andrew S.
APPLICANT: Kande, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 47.7%; Score 527.5; DB 2; Best Local Similarity 52.4%; Pred. No. 1.9e-50; Matches 97; Conservative 45; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         Sequence 25, Application US/08531525 Patent No. 5840683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ferber, Donna M.
RECISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                     181 RMRASNE 187
                                                                                                                                                            181 SPQGSNQ 187
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CITY: Boulder
'STATE: Colorado
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ORGANISM: Car
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                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                        NKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                  1 MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ 60
MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09198184
Patent No. 6010595
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
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APPLICATION NUMBER: 08/824,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: B1111ngs, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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                                                                                                                                                                                                                                                                            181 SPQGSNQ 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GenBank
CLONE: 234746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-09-198-184-4
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                 APPLICANT: "Lavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 5840681e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
TITLE OF INVENTION: 0; P21 Ras
NUMBER OF SEQUENCES: 52
CANRESPONDENCE ADDRESS:
ADDRESSEE: Greenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8e-49;
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                                                                                                                                                                                                                 Sequence 51, Application US/08531525
Patent No. 5840683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 37-9
REFERENCE/POCKET NUMBER: 37-9
TELECOMMUNICATION INFORMATION:
TELEFORE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Canis familiaris US-08-531-525-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.0%
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colorado
                                                                              RASNE 187
                                                                                                                181 QGSNQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boulder
STATE: Colorade
COUNTRY: US
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121 CDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGNSP 180
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                                                                                                                                                                   Sequence 25. Application US/08718270A
Patent No. 5910478
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Abajian, Henry B.
APPLICANT: Rende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF INVENTION: The Oncogenic Action of F21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.7%; Score 527.5; DB 2; Best Local Similarity 52.4%; Pred. No. 1.9e-50; Matches 97; Conservative 45; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREEF: 5370 Manhattan Circle, Suite 201 CITT: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21.5E9-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5E9-1995
ATTOMNEY GENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPRAN: (303) 499-8080
TELEPRAN: (303) 499-8089
INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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181 QGSNQ 185
                                    183 RASNE 187
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ORGANISM: Can
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Sequence 35, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Hlavka, Joseph J.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Rende, Andrew S.
TILLE OF INVENTION: Deptides Inhibiting the Oncogenic Action
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Greenlee and Winner, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%; Score 503.5; DB 2; 46.4%; Pred. No. 8.8e-48;
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56; Mismatches 44
                                                                                                                                                                                                                                                                            ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201 CIIY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 RASNELALAE-LEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 37-9
REFERENCE/DOCKET NUMBER: 37-9
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 antino acids
TYPE: antino acid
STRANDEDNESS: single
STRANDEDNESS: single
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NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,
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Best Local Similarity 46.49
Matches 96; Conservative
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 80303
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US-08-531-525-35
US-08-531-525-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || | | : || | : :|:|:|:|:|:|:|:|:|:|:|| | :|::| | | :|::|
NKCDMDDKRVVPKGKGEQIAREHGIRFFETSAKVNINIEKAFLTLAEDILR 170
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                                                APPLICANT: Hlavka, Joseph J.
APPLICANT: Hlavka, Joseph J.
APPLICANT: No. 59104781e, John F.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Abajian, Henry B.
TITLE OF INVENTION: Peptidomimetics Inhibiting: TITLE OF INVENTION: Peptidomimetics Inhibiting: NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STREET: 5370 v---
CTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-SEP-1996
CLASSIFICANION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 1-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY-AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 78-95
ATTORNEY-AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
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nes 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORIGINAL SOURCE:
) ORGANISM: Canis familiaris
US-08-718-270A-51
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amino acid
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                    Colorado
                                                                                                                                                                                                                                                                                                                                                                           CITY: Boulder STATE: Colorac
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 80303
                                       JS-08-718-270A-51
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62 DTAGQERFRITT-AYYRGAMGIMKV-DITNEKSFDNIKNWIRNIEEHASSDVERMILGNK 119
                                                                                                                                                                 63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                              123 ADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                      120 CDMNEKROVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKM---- 174
3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                              2 KIYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNITFISTIGIDFKIRTVELDGKKIKLQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-718-270A-35; Sequence 35, Application US/08718270A; Patent No. 5910478; DENERAL INFORMATION:
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RESULT 7

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Hlavka, Joseph J.
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STREET: 55.0
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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US-08-718-270A-10
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                                        APPLICANT:
APPLICANT:
APPLICANT:
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                      GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 DTAGQERFRITT-AYYRGAMGIMKV-DITNEKSFDNIKNWIRNIEEHASSDVERMILGNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KTYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNTTFISTIGIDFKIRTVELDGKKIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.6%; Score 503.5; DB 2; Length 2
Best Local Similarity 46.4%; Pred. No. 8.8e-48;
Matches 96; Conservative 56; Mismatches 44; Indels
                                                                     APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF INVENTION: the Oncogenic Action of P21 Ras
WUMBER OF SOUGHNES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              SULTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION:
                                                                                                                                                                          ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NENSLQEAVDKLKSPPKKPSQKKK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 RASNELALAE-LEEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Pincus, Matthew R.
No. 59104781e, John F.
Abajian, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-531-525-10 Sequence 10, Application US/08531525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8089
INFORMATION FOR SEO ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Discopyge ommata
US-08-718-270A-35
Joseph J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
  Hlavka,
                                                                                                                                                                                                                 CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                          80303
                                                                                                                                                                                                                                                   COUNTRY:
                  APPLICANT:
APPLICANT:
APPLICANT:
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72 AGQER-RITITAXYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 MDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIG------RDIKQR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 19;
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 215;
                                                                                                                                                                                                                                                                                                                                               SUFTWARE: PC-DOS/MS-DOS
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/531,525
FILING DATE: 21-SEP-1995
ATTORNEX/AGENT ... 530
ATTORNEX/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
44.8%; Score 494.5; DB 2;
Best Local Similarity 46.9%; Pred. No. 9.2e-47;
Matches 100; Conservative 40; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08718270A Patent No. 5910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ferber, Donna M.
REGIZTRATION NUMBER: 33,878
RERERCCHOCKET.NUMBER: 37-9.
TELEPHONE: (303) 499-8080
INFORMATION SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
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amino acid
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ATTOCHEN NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIPICATION: 530
ATTOCHEV, CASENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 37-94
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08718270A
Patent No. 5910478
                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICATION NUMBER: US,
FILING DATE: 21-SEP-19
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                  CITY: Boulder
STATE: Colorado
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                                                                                                                                                                                                                                                                                                80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.8%; Score 494.5; DB 2; Length 215; 46.9%; Pred. No. 9.2e-47; tive 40; Mismatches 54; Indels 19
                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION 514
PRIOR APPLICATION BTA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTONENEY/AGENT IRPORMATION:
ANAMERICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTONEX/AGENT IRPORMATION:
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Rende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                E: Greenlee, Winner and Sullivan, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
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180 LSDTDSRAEPATIKISQTDQAAGAGQATQKSAC 212
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Patent No. 5840683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thallana US-08-718-270A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMULCATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 and no acids
TYPE: amino acids
STANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.93
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                   ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                              Colorado
                                                                                                                                                                        STATE: Colder
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                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                      STREET:
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
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APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abalian, Henry B.
APPLICANT: Rende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action NUMBER OF SEQUENCES: 52
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 194;
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GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF INVENTION: the Oncogenic Action of P21 Ras
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 44.2%; Score 488.5; DB 2; Best Local Similarity 55.8%; Pred. No. 3.6e-46; Matches 96; Conservative 41; Mismatches 30;
                                                                                                                                                                                                                                                       ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LIBRARY: LIVRTUT04
; CLONE: 2514506
US-08-916-901-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                               FILING DATE:
                                       94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GNKADEEOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRILICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
                   E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.2%; Score 488.5; DB 2
55.8%; Pred. No. 3.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches
                                                                                                                                                                                                                                                          CLASSIFICATION: 514

RICH APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21.5EP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      33,878
ER: 78-95
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; Sequence 3, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Discopyge ommata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.8%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
   CORRESPONDENCE ADDRESS:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                    CITY: Boulder
STATE: Colorado
                                                                                                        80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-718-270A-34
                  ADDRESSEE
                                                                                    COUNTRY:
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 478.5; DB 2; Length 2; Pred. No. 4.9e-45; 42; Mismatches 64; Indels
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RMRASNELALAELEEEEGKPEG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GAASGERPNLKIDSTPVKPAG 197
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                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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Best Local Similarity 45.0%;
Matches 91; Conservative 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.3%; Score 478.5; DB 4
Best Local Similarity 45.0%; Pred. No. 4.9e-45;
Matches . 91; Conservative 42; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PESTSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TILLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                             PF-0367 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 GAASGGERPNLKIDSTPVKPAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RMRASNELALAELEEEEGKPEG 202
                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/916,901
                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION UNDRER: 36,749
REFERENCE/DOCKET NUMBER: PF-03
REPERPHONE: 415-85-0555
TELEFONMUNICATION INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08916901
Patent No. 5892012
                                                                                                                                                                                                                                                                                                                                       LENGTH: 201 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: LIVRTUTO4
CLONE: 2514506
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                       FILING DATE:
                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-154-602-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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June 18, 2003, 15:35:37 ; Search time 49 Seconds (without alignments) . 468.160 Million cell updates/sec
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1105
1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKFBGPANSSKTCWC 212
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                417779 seqs, 108206813 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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/cgn2_6/ptodata/2/pubpaa/DCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* ptodata/2/pubpaa/US10_NEW_PUB.pep:* /cgn2_6,

Published_Applications_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Suery Match Length DR	E C	£	Description
i				1		
Н	1105	100.0	212	10	US-09-817-198A-2	Sequence 2, Appl1
7	1105	100.0	401	6	US-09-764-868-701	Sequence 701, App
٣	1092	98.8	218	10	US-09-817-198A-5	Sequence 5, Appli
4	1077	97.5	212	10	US-09-817-198A-4	Sequence 4, Appli
Ŋ	832	75.3	188	6	US-09-764-868-1120	Sequence 1120, Ap
9	532	48.1	246	10	US-09-925-302-534	Sequence 534, App
7	530.5	48.0	218	10	US-09-925-300-1571	Sequence 1571, Ap
8	528.5	47.8	207	10	US-09-794-257-8	Sequence 8, Appli
σ	512	46.3	190	유	US-09-822-860-5	Sequence 5, Appl1
2	497	45.0	162	10	US-09-834-765-766	Sequence 766, App
⊒	478.5	43.3	201	10	US-09-967-736-3	Sequence 3, Appli
2	478.5	43.3	224	σ	US-10-102-806-466	Sequence 466, App
13	469	42.4	201	10	US-09-967-736-8	Sequence 8, Appl1
14	467	42.3	222	10	US-09-820-003A-4	Sequence 4, Appli
15	434.5	39.3	198	10	US-09-794-257-16	Sequence 16, Appl
16	434.5	39.3	198	10	US-09-945-173-5	S
17	434.5	39.3	198	2	US-09-972-529-4	
18	430	38.9	223	10	US-09-817-199A-4	Sequence 4, Appli
61	429	38.8	223	10	US-09-817-199A-2	Sequence 2, Appli

121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180

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181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212

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RESULT

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ORGANISM: Rattus norvegicus
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SEO ID NO 1120
LENGTH: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-764-868-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-817-198A-4
                                                                                                                                             US-09-817-198A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKADEEQKRQVGREGGG-----QLAKEYGMDFYETSACTNLNIKESFTRLFELVLQAHR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                              27 MAKQIDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YE, Jame et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

CURRENT PELLING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                    Length 401;
         Sequence 701, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                Query Match

100.0%; Score 1105; DB 9; Length
Best Local Similarity 100.0%; Pred. No. 8e-96;
Matches 212; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 6.2e-95;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09817198A Patent No. US20020146758A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.8%;
Best Local Similarity 97.2%;
Matches 212; Conservative
                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-764-868-701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
US-09-764-868-701
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                                                                                                                                                                                                                       SEQ ID NO 701
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/REY: SITE
LOCATION: (151)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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Patent No. US20020168711A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVERTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUBER: US/09/764,868
CURRENT APPLICATION DATE: 2001-01-17
PRIOR APPLICATION DATE: 2001-01-17
PRIOR APPLICATION DATE: 1500-01-17
WUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                           181 KELEGLIAMRASNELALAELEEEGKPEGPANSSKTCWC 218
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                                                                 175 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC
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2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                Sequence 4, Application US/09817198A Patent No. US20020146758A1
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Best Local Similarity 97.6%;
Matches 207; Conservative :
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Query Match
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LOCATION: (161)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                    : LOCATION: (188)
; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1120
                                                                                                                                                                                                                                                                                                                                        44 MAKAYDHLEKLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTYDIEGKKIKLQ 103
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                                                               LOCATION: (164)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (188)
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                                                                                                                                                                                                                       0; Gaps
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Patent No. US20200044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2009-03-12
NUMBER OF SEQ ID NOS: 896
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                 Score 832; DB 9; Length 188;
Pred. No. 1.4e-70;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RMRASNELALAELEEEEGKPEGPANSSKTC 210
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                                                                                                                                                                                 Query Match 75.3%;
Best Local Similarity 97.6%;
Matches 160; Conservative
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Best Local Similarity 47.6%;
Matches 100; Conservative 4
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US-09-925-302-534
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LENGTH: 246
TYPE: PRT
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APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel
TITLE OF INVENTION: Human G-Froteins
TITLE DESERBNCE: 35800/20928
TITLE REFERENCE: 35800/20929
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASKESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWYSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 218;
                                                            APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SEQ ID NO 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 530.5; DB 1
55.8%; Pred. No. 3.6e-42;
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; Sequence 8, Application US/09794257
; Patent No. US2002009804A1
; GENERAL INFORMATION:
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Best Local Similarity 54.0%;
Matches 95; Conservative 4
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Matches 96; Conservative
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
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LENGTH: 207
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APPLICANT: ZHU, Shiaoping et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001214
CURRENT APPLICATION NUMBER: US/09/822,860
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRESEG FOR WINGOWS VERSION 4.0
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APPLICANT: PlA M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILLE REFERENCE: 129.60501
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Pred. No. 1.6e-40;
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V 47.7%; Pred. No. 1...
'... 52; Mismatches
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                                  Sequence 5, Application US/09822860 Patent No. US20020146795A1
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.77
Matches 93; Conservative
                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Discopyge ommata
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Best Local Similarity
Matches 87; Conserv
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                 US-09-822-860-5
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Gaps

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                                                                                                      RYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKADEEQK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                      9 FRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDTAGQE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                              ROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.3%; Score 478.5; DB : 45.0%; Pred. No. 2.5e-37, tive 42; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CURKNOWN ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                              Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L. Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09967736 Patent No. US20020103340A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 201 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: LIVRTUT04
CLONE: 2514506
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
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Best Local Similarity
Matches 91; Conserv
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SEQ ID NO 4
LENGTH: 222
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8-981-136-8
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                       IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAF-----MTMAAEIKKRMGP 198
NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLFELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 224;
                                                                                                                                                                                                   Sequence 466, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%; Score 478.5; 45.0%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 RMRASNELALAELEEEGKPEG 202
                                                                     181 RMRASNELALAELEEEGKPEG 202
                                                                                              GAASGGERPNLKIDSTPVKPAG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09967736 Patent No. US20020103340Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lal, Preeti
Corley, Neil C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 466
LENGTH: 224
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CORGANISM: Homo sapiens
US-10-102-806-466
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ZIP: 94304
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Best Local Similarity
Matches 91; Conserv
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US-10-102-806-466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF 162
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 467; DB 10;
Pred. No. 3.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 469; DB 10;
Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                             PF-0367 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-5ep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/820,003A CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                        APPLICATION NUMBER: 09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09820003A Patent No. US20020142382A1
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 201 amino acids
                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.2%; Promatches 83; Conservative 36;
                                                                                                                                                                                                                                                                                                                              ELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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51.9%;
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Best Local Similarity 51...
Local 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
CLONE: 57006
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Sequence 16, Application US/09794257

Patent No. US20020009804A1

GENERAL INFORMATION:

APPLICANT: Meyers. Rachel

TITLE OF INVENTION: 32705, 23224, 27423, 32712, No. US20020009804A1e1

TITLE OF INVENTION: JANUAR G-Proteins

TITLE OF INVENTION: Human G-Proteins

FILE REFERENCE: 35800/209285

CURRENT APPLICATION NUMBER: US/09/794,257

CURRENT FILING DATE: 2001-02-27

PHIOR APPLICATION NUMBER: 60/185,606

PHIOR PAICATION AUGUST: 6000-02-29

NUMBER OF SEQ ID NOS: 16

SEQ ID NOS: 16

SEQ ID NO 16

LENGTH: 198
                           61 FRALRPAYYRGAQGFLLVYDITSRDSFENVKKWLEEILRHADKDENVPIVLVGNKCDLED 120
61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 YQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYA--PEGVQKILLGNKAD--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 RLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDTAGQER 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
39.3%; Score 434.5; DB 10; Length 198;
Best Local Similarity 50.9%; Pred. No. 3.3e-33;
Matches 89; Conservative 30; Mismatches 43; Indels 13;
                                                                                       121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF 162
                                                                                                                        FEATURE:
CTHER INFORMATION: Pfam accession number PF00071
US-09-794-257-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Search completed: June 18, 2003, 15:44:58 Job time : 50 secs

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June 23, 2003, 10:45:22; Search time 2485 Seconds (Without alignments) 2482.815 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                             - nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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1105
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Sequence:
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                                                                                                                   Run on:
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4109280 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

2054640 seqs, 14551402878 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Command line parameters:

MODEL-frame+_practs:
-OMMINICATE PROMOCAS.
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em_sts:* em_un:* em_fun:* em_hum: gb_ba:*
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em_v1:*	em_htg_hum:*	em_htg_inv:*	em_htg_other:*	em_htg_mus:*	em_htg_pln:*	tg.	em_htg_mam:*	em_htg_vrt:*		em_htgo_hum:*	em_htgo_mus:*	em htgo other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	c	CO000CAK	CCG	S 67420M	BC01379	AB006189	AY060425	AF498943	.sapie	X56385 Ca	ВС002977 Ношо	AK025165 HOMO		M38391 Discopy	BC000799	Х75593 Н.	AF498948 Homo sar	M38390 D18copy	C AFZ9/66U HOMO Sapi	X56387 Canine	AF035646 Mus	вс000896 ношо	Ношо	AK023223 Homo	D01025 Arabidopsi	5 AYU42/95 Arabidops 2 AYU35132 Arabidops	AX236078	5 053475	0 AF525280	BC020654	AX236076		D84347 DT	AX285074 Sequence	AX285080	AX285089	AX285091	AK001111	8 AL833365	Z73948 L. japon	0 AL136650	S53270 MEL=RAS-rel
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Mammalia; Eutheria; F
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ACA_xxef="G1:21336158"
//translation="ARKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFRMATIEVDGIKVRIQIMDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVFRMATIEVDGIKVRIQIMDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVFRMATIEVDGIKANDEBORRQVGREQGOLAKEYGMDFYETSACTMLNIKESTRALTLULQAHRKELEGIRMRASNELALBELEBEBGKREGPANSSKTCWC"
1314 c 1 others
               PAT 06-JUN-2002
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Patent: WO 0218424-A 74 07-MAR-2002;
HYSEQ, INC. (US)
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Catarrhini; Hominidae; Homo.
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Mismatches:
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Sequence 74 from Patent WO0218424.
AX399903
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs.refmail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgir.nih.gov/
Contact: nisc.mgc@nhgir.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspl.R.,
Maduro,O.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC027769 3139 bp mRNA linear ROD 07-AUG-2002
Mus musculus, clone MGC:38375 IMAGE:5345297, mRNA, complete cds.
BC027769
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGluGluGlyLysPro
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SFTRLTELVLQAHRASNELALAELEEDEGKPEGPANSSKTCWC"
847 c 878 g 691 t
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Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
M83679.
M83679.1 GI:206536
LWM GTP-binding protein.
Rattus norvegicus (strain Sprague-Dawley) (library: LAMBDA ZAPII)
Rattus norvegicus
Rattus norvegicus
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Rattus norvegicus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleGlyValAspPheLySMetLySThrIleGluValAspGlyIleLySValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                         protein
l (bases 1 to 945)
Elferink.L.A., Amzai.K. and Scheller,R.H.
rabls, a novel low molecular weight GTP-binding
specifically expressed in rat brain
92.1051. Chem. 267 (9), 5768-5775 (1992)
1313420
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207
0
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Matches:
Conservative:
Mismatches:
                                                                                                         norvegicus"
                                                                                                                                                                ZAPII"
                                                                                                                /strain="Sprague-Dawley"
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-945)
                                                                              Location/Qualifiers
1. .945
/organism="Rattus no
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-817-198B-2 (1-212) x RATRAB15X
                                                                                                                                                                                                 220. .858
/gene="RAB15"
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                                                                                                                                                                                      /gene="RAB15"
220. .858
                                                                                                                                                                                                                                                                                                                                                                  1.12e-97
1077.00
98.58%
97.64%
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DEFINITION ACCESSION VERSION

RESULT 4 BC013790

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à g ò ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

REMARK COMMENT

FEATURES

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AsnLysAlaAspGluGlnGlnLysArgGlnValGlyArgGluGlnGlnGlnCnleuAla 140
                                                                                                                                                                                                                                                                                                                                                              214 AAGACATGCCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 273
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Direct Submission
Direct Submission
Submitted (01-040-1997) Koichi Ozaki, Osaka University, Graduate
Submitted (01-040-1997) Koichi Ozaki, Osaka University, Graduate
School of Science, Department of Biology; 1-1 Machikaneyama,
School of Science, Dapar (E-mail:ozaki@bio.sci.osaka-u.ac.jp,
Toyonaka, Osaka 560, Japan (E-mail:ozaki@bio.sci.osaka-u.ac.jp,
Tel:+81-6-850-5439, Fax:+81-6-850-5439)
Location/Qualifiers
                                                                                                                                                                                                                                    LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                        41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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Satol,A.K., Tokunaga.F. and Ozaki,K.
Rab proteins of Drosophila melanogaster: novel members of the
Rab-protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (strain:Oregon R) head cDNA to mRNA
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Conservative:
Mismatches:
                                                                                                                                    Indels:
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Drosophila melanogaster
AB006189
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Rab10.
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100.008
99.358
72.228
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                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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                                               Pred. No.:
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                              Alignment
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                                                                                                                                                                                                                                                          Mus musculus, clone MGC:6897 IMAGE:2655151, mRNA, complete cds. BC013790. G:15489393 MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 5 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.

Location/Qualifiers
1. 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Unknown (protein for MGC:6897)"
/protein_id="AAH13790.1"
/db_xref="G1:15489394"
/translation="MAKQYDVLFRLLLIGDSGVGRTCLLCRFTDNEFHSSHISTIGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKMKTIDVDGIKVRIQIWDTAGQERYQTITKQYYRRAGGIFLVYDISSERSYQHIMKW
VSDVDEYAPEGVQXILIGNKADEEQKRQVGREQGQLAKEYGMDFYETSACFFSSFFS
/tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam2" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus Sukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro
                                                                                                                                                                     GluGlyProAlaAsnSerSerLysThrCysTrpCys 212
                                                                                                                                                                                           820 GAAGGCCCAGCAAACTCTTCAAAGACCTGCTGGTGC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MGC:6897 IMAGE:2655151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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BASE COUNT ORIGIN

INV 07-AUG-1997

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US-09-817-198B-2 (1-212) x AY060425 (1-2349)
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Drosophila melanogaster
              AY060425
AY060425.1 GI:16648397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Rab10"
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                                                   SOURCE
                                                                                                            /translation="MAKKTYDLLFKLLLIGDSGVGKTCILFRFSDDAFTSTFISTIGI
DEKKTYDELGGKKIKLQIWDTAGQBREHTITTSTYRGAMGIMLYYDJTNBKSFENIYK
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RAFCELLABALLDKTSGRESAENDEWYIDRRNQEKAEGYSKCCA"
365 c 430 g 358 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuile 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 GluSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGly 179
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                                                                                                                                                                                                                                                                                                                                      257 ATGGCAAAGAAAACCTACGATTTGCTCTTTAAACTGTTGCTGATCGGTGATTCAGGAGTG
                                                                                                                                                                                                                                                                                                                                                                        GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                                                                                                                                                                                                                                                                                                     40 ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu
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185 CGCGAGTCGGCGGAATCAGCAGCGCGTGATTATCGATCGCCGGAACCAGGAAGGCG
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Matches:
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location (http://fruitfly.berkeley.edu) or send email to candaffullity.berkeley.edu.
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DEK KTYDELGKKIKLQIMDTAGQERFHTITISYYRGAMGIMLYYDITNEKSFENIYK
WIRNIDEHANEDVEKMILGNKCDMTDKRYVNKERGEAIAREHGIRFWETSAKSNINIE
RAFCELABALILDKTSGEAENQERVIIDRRNQEKAPGYSKCCA"
                                                                                                                                                                                                                                                                                                                                              Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarlin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Parks, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rublin, G.M. and Celniker, S. Dhouanenavong, S., Wan, K., Direct Submitselon (20 CGT-2001) Berkeley Drosophila Genome Project, Barkeley, CA 94720, USA Sequence Submitted by:

Berkeley, CA 94720, USA
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley CA 94720
                                                                                                                                                                                                                 Insecta; Pterygota;
                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Moptiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2349)
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Drosophila melanogaster LD39986 full length cDNA
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Mismatches:
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/db_xref="FLYBASE:FBgn0015789"
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/protein_id="AAL25464.1"
/db_xref="G1:16648398"
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/db_xref="taxon:7227"
/map="19C1-19C1"
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/gene="RAB8"
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                                                                                                            BASE COUNT
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                                                                                                                                                                                                                                                                   GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
                                                                                                                                                                                                                                                                                                             AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                                                                                                                                                                                                                                                                                                                                                      434
                                                                                                                                              MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                     675 GCCCGTGAACATGGCATTCGGTTTATGGAAACATCCGCCAAGTCGAACATAAACATCGAG 734
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                                                                                                                                                                                                                                                                                                                                                                                                    180 LeuargMetargalaSerasnGluLeualaLeualaGluLeuGluGluGluGluGlyLys 199
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
 19
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Publ.H.L. III, Ikeda,S.R. and Aronstam,R.S.
Direct Submission
Submitted (05-ARR-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
Location/Qualifiers
                                                                                      GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                            20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                                                                                              80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
  MetalaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal
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Publ.H.L. III, Ikeda,S.R. and Aronstam,R.S.
Gopublished
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="brain"
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AF498943.1 GI:20379061
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Homo sapiens
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AUTHORS
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AUTHORS
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JOURNAL
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/product="small GTP binding protein RAB8"
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/protein_id="AAM21091.1"
/protein_id="AAM21091.1"
/db_xxef="cd::203790612"
/translation="MAKTYDYLE"
/translation
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="RAB family member"
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rab-related GTP-binding protein.
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X56741
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                                      /codon_start=1
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77.01%
52.94%
49.32%
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LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160

431 CTCGACTATGGAATCAAGTTCATGGAGACCAGCGCGAAGGCCAACATCAATGTGGAAAAT SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu

180 550

191

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                                          Submitted (26-NOV-1990) A. Zahraoui, INSERM-U 248, 10 AVENUE DE 2 (bases 1 to 660) at 1 to 660.

Tahraoui, A., Joberty, G., Arpin, M., Fontaine, J.J., Hellio, R., Asmall rab Grpase is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker 20-1 in polarized epithelial cells
J. Cell Biol. 124 (1-2), 101-115 (1994)
                                                                                                                                                                                                                                                                                                        /codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 660)
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                                                                                                                                                                                         Location/Qualifiers
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                      Zahraoui, A.
Direct Submission
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AFFILMEDIKARMSLLGGNSPOGSNGVKITPDQQRRSSFFRCVLL"
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Canis.
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Submitted (17-AUG-1990) Zerial M., EMBL, Meyerhofstrasse 1, 6900
Heidelberg, FRG
                                                                                                                                                                                                                                Chavrier, P., Vingron, M., Sander, C., Simons, K. and Zerial, M. Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ras gene
                                                                                     760 bp mRNA linear M rab8 mRNA for ras-related GTP-binding protein.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
1 (bases 1 to 760)
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1. 760
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                 AGCCCCCAGGGGAGCAACCAG
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GTP-binding protein; p.
Canis familiaris.
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Email: cgapbs-r@mail.nih.gov
Contact: MCC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticla Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Scheln, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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Homo sapiens, mel transforming oncogene (derived from cell line
NKI4)- RAB8 homolog, clone MGC:2196 IMAGE:3547214, mRNA, complete
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-FEB-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                           IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                     AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
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| AACAAGTGTGATGTGAACGACAAAGATTTCCAAGGAACGGGGGAGAAAAGCTGGCC
IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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BC002977.1 GI:12804236
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Strausberg, R.
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/product="mel transforming oncogene (derived from cell line NR14) - RABB homolog" /protein_id="AAH02977.1" /db.xref="Gr.12804237" /db.xref="Gr.12804237" /translation="MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID FRIRTIELDGKRIKLOMDTAGQERFRTITTAYYRGAMGIMLYYDTINEKSFDNIRNW IRNIEBHARDMKKLEGNSPQGSNGGVKITPDQQKRSSFFRCVLL" 556 c 493 g 467 t
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 452317.

Location/Qualifiers
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                                                                                                                      1. .2048

/organism="Homo sapiens"

/db_xref="Locus1D:4218"

/db_xref="taxon:9606"

/clone="MGC:2196 IMAGE:3547214"

/tissue_type="Skin, melanotic melanoma."

/clone_lib="NIH_MGC_20"

/lab_host="Db110B-R"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROD 07-AUG-2002
                                                                                                                                                                                                                                                                                AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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126 ATATGGGACACACGCGGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACAGGGGT 485
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1337)
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S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIAN_at: http://image.llnl.gov Series: IRAK Plate: 37 Row: c Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                           666 CTCGACTATGGAATCAAGTTCATGGAGACCAGCGCGAAGGCCAACATCAATGTGGAAAAT
                                                                                                                  101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: The Technologies, Inc.
CDNA Library Prayade Dy: The I. M.A.G. E. Consortium (Linl.)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly'
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart.
Richards, S., Gibbs, R.A.
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/db_xref-"taxon:10090"
/map-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ArgMetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       786 AGCCCCCAGGGGAGCAACCAG 806
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BC019990.1 GI:18043408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       Rawabata,A, Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Swancto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blotechnology; cDNA library construction, 5' & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
                                                                                                                                                                                                        oligo capping; fis (full insert sequence).
Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL05769.
Homo sapiens
                                                                                                                                       clone COL05769.
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                                                                                                                              2818 bp
Homo sapiens cDNA: FLJ21512 fis,
AK025165
Oligo canning
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                181 ArgMetArgAlaSerAsnGlu 187
                                                      617 AGCCCCCAGGGGAGCAACCAG 637
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Best Local Similarity:
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                                                                                                 RESULT 11
                                                                                                                  AK025165,
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                                                   /codon_start=1
//codon_start=1
//product="Similar to mel transforming oncogene (derived //product="Similar to mel transforming oncogene (derived //product="Similar NabB homolog"
//protein_id="AAH19990.1"
//db_xref="GI:|B043409"
//translation="MAKTYDYLEKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID FRIREIEDGKRIKAQIMPAGOERRATITTARYRGAMGIMLYYDTINEKSFONIRNW IRNIEEHASADVEKMILGNKCDVNDKRQVSKERGEKLALDYGIKFMETSARANINVEN AFFTLARDIRARMDRKLBGNBSQGSSHGVKITYPEQQKRISFFRCSLL"
338 c 341 g 291 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          month old male mouse."
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999
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Matches:
Conservative:
Mismatches:
Indels:
/tissue_type="Liver, normal. 5
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                  /note="Vector: pCMV-SPORT6"
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/translation-"MAKTYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNTTFISTIGID
FRIETVELDGKKIKLGIWDYAGGERFRITTAYYRGAMGIMKYYDITNEKSFDNIKNW
TRIIEFHASSDVERMILGANCOMNERRQVSKERGEKLAIDYGIKFLETSAKSSINVEE
AFTITLANDIMTKENNENSLQEAVDKLKSPPKKPSQKKKQLSFRCSLL"
165 c 175 g 168 t
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoldel; Narcinidae; Discopyge.

1 (bases 1 to 765)
Ngsee,J.K., Elferink,L.A. and Scheller,R.H.
A family of ras-like GTP-binding proteins expressed in electromotor
                                                                                                                                                                                          neurons
Unpublished (1990)
Draft entry and computer-readable sequence for [1] kindly submitted
by J.K.Ngsee, 10-SEP-1990.
Dept of Biological Sciences
                                                                                                                                                                                                                                                                                                                Stanford University
Stanford, CA 94305-5020
Braff entry and computer.readable sequence for [1] kindly submitted
by J. K. Ngsee, 10-SEP-1990.
Dept of Biological Sciences
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GTP-binding protein.
D.ommata electric lobe electromotor neuron,
Discopyge ommata
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Matches:
Conservative:
Mismatches:
Indels:
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/protein_id="AAA49232.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Discopyge ommata'/db_xref="taxon:7785"
/cell_type="electromotor neu/tissue_type="electric lobe'/
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Stanford, CA 94305-5020.
Location/Qualiflers
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539.50
74.16%
47.37%
48.82%
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/product="RAB13, member RAS oncogene family"
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Best Local Similarity:
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oncogene family, clone MGC:5074
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                        AsniysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                          141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                        SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
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                                                                                                                                                                                                                                                                       ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGlu---LeuGluGluGluGluGlyLys 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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GCATTTATTACACTTGCACGAGATATCATGACGAAAACTCAACAAGAAAATG------
     LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_l0"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
95. .706
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Homo sapiens, RAB13, member RAS on
IMAGE:3451945, mRNA, complete cds.
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590 CCAAAGAAACCCAGTCAAAAAGAAAAAG 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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BC000799.1 GI:12654002
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TITLE
JOURNAL
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                                                                                                                                                          MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGly
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                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1238)
Zahraoui,A., Joberty,G., Arpin,M., Fontaine,J.J., Hellio,R.,
Tavitian,A. and Louvard,D.
Positian,A. Joberty,G., Arpin,M., Fontaine,J.J., Hellio,R.,
Tavitian,A. and Louvard,D.
Positian,A. and Louvard,D
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APSSSLAMADILLKGGRRSGNNGWKPPSTDLKTCDKKNTNKCSLG"
275 c 355 9 244 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-NOV-1993) A. Zahraoui, INSERM U.248, 10 Avenue de Verdun, 75010 Paris, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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Matches:
Conservative:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="CaCO2"
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/db_xref="G1:452320"
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Zahraoui,A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                      ---- GlnAlaHisArgLysGlu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                          739 CICCCIGGCIGAGGACCCITICITGCCTCCCCACCCGGAAGCIGAACCIGAGGGAGA 798
440 AACTGGATGAAAAGCATCAAGGAGAATGCCTCGGCTGGGGTGGAGCGCCTCTTGCTGGGG
                                                                                    141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
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620 GCTTTTAGTTCCCTGGGCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGGAAAC
                                                                                                                                                                                                                                                                                                                                                          680 GGCAACAAGCCTCCCAGTACTGACCTGAAAACTTGTGACAAGAAGAA-CACCAACAAGTG
                                                       121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnLeuAla
                                                                                                                                                                                                                                161 SerPheThrArgLeuThrGluLeuValLeu---------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 GluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrp 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
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Search completed: June 23, 2003, 11:52:37 Job time: 2491 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 23, 2003, 03:05:27; Search time 227 Seconds (without alignments) 2103.188 Million cell updates/sec
OM protein - nucleic search, using frame_plus_p2n model
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1105 1 MAKQYDVLFRLLLIGDSGVG......LEEBEGKPEGPANSSKTCWC 212 2185239 seqs, 1125999159 residues 0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-817-198B-2 BLOSUM62 Perfect score: Sequence: Scoring table:

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Searched:

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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ALIGNMENTS

ВÞ AAS27053 standard; cDNA; 2021 AAS27053;

RESULT 1 AAS27053

(first entry) 07-NOV-2001

chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; Neuroprotective, cytostatic, dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; cDNA encoding novel signal transduction pathway protein, Seg ID 88.

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2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000;
reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                              17-JAN-2001; 2001WO-US01312
                         WO200154733-A1
                                                                              16-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                                                              19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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05-SEP-2000;
05-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
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22-AUG-2000;
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23-AUG-2000;
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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and diseases including immune system disponsing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases transplant rejections and graft versus host disease, infectious diseases. C. e.g. hepatitis (2), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders; in wound healing, epithelial cell proliferation, endocrine disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodiess, and as means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction bathway protein coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                              Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 88; 880pp; English.
                                                                                                        Ruben SM;
                                                     (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678.
                                                                                                     Barash SC,
                                                                                                                                                   WPI; 2001-465460/50.
P-PSDB; AAU17136.
                                                                                                     Rosen CA,
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2021 212 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-817-198B-2 (1-212) x AAS27053 (1-2021) 6.03e-118 1105.00 100.00% 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: .. ov Score: Pred ò

AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100 41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln 60 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 21 201 261 61 101 381 81 321 a δ 셤 à ద ò g ð g å

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX

Claim 5; Page 1978-1979; 5507pp; English.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Shimkets RA, Leach M; (CURA-) CURAGEN CORP.

260

80

320

WPI; 2000-602362/57. P-PSDB; AAB41604.

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200
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                                                                                                    180
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                                                                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; antivirant; antibacterial; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiantemnic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID: AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                  LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
                                                               AsnLysAlaAspGluGluGlnLysArgGlnNalGlyArgGluGlnGlyGlnGlnLeuAla
              Human ORFX ORF1368 polynucleotide sequence SEQ ID NO:2735.
                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                 AAC75813 standard; cDNA; 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000WO-US08621.
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121
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sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiametrory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic ansemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
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511 CCTTCTCTTCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 LysGluLeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGlu 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArg 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                      21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                         AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGln-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluGluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrpCys 212
Sequence 1666 BP; 333 A; 529 C; 461 G; 341 T; 2 other;
                               Length:
Matches:
Conservative:
Mismatches:
                                                                          Indels:
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Best Local Similarity:
Query Match:
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antiliflammatory; anti-HIV; antibacterial; antiliflammatory.cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality; bown syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; ss;
                                                                                                                    cDNA encoding novel signal transduction pathway protein, Seq ID 507.
Neuroprotective; cytostatic; dermatological; immunosuppressive;
                                                                                                                                                                                                                                        acquired immune deficiency syndrome.
                                                   AAS27472 standard; cDNA; 566
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                                                                                                (first entry)
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2000US-0249216
        06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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113-SEP-2000;
14-SEP-2000;
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27-SEP-2000;
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01-NOV-2000;
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25-SEP-2000
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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant replections and graft versus host disease, infectious diseases transplant replections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, infectious diseases (e.g. hepatitis C), bleeding disorders; hyperproliferative disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. disease), chromosomal solutions (e.g. disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal clasorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. arrhythmia), respiratory disorders, disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 507; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                   2000US-0249300
2000US-0250160
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P-PSDB; AAU17555.
          17 - NOV - 2000;
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17-NOV-2000;
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06-DEC-2000;
08-DEC-2000;
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05-JAN-2001;
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Alignment Scores:

Pred. No.:

832.00

Matches:

Percent Similarity:

97.56%

Mismatches:

75.29%

Migels:

22.63

Maches:

Mismatches:

23.64

Mismatches:

24.66-87

Matches:

Mismatches:

25.29%

Mismatches:

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US-09-817-198B-2 (1-212) x AAS27472 (1-566)

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insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                           Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                     LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
        LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                       IleGlyValAspPheLySMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                             NO 34594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 34594; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide
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                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                               DNA; 1540
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                       SerPheThrArg 164
                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                               ABL27707 standard;
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                                                                                                                                                                                                                                                                                                                                           Drosophila;
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                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaLysCluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal
                                                                                                                                                                                                                                                                                                                                                                                               GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                      Sequence 1540 BP; 437 A; 353 C; 420 G; 330 T; 0 other;
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Conservative:
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546.50
72.04%
49.76%
49.46%
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contribon also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have bomology to known proteins, thereby giving an insight into their probable biological activities, and hence of polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to potential therapeutic applications. The polypeptides of the invention activities; stem cell growth activity; have activity; have activity; itssue growth activity; have activity; have activities; chemotactic or chemothactic activities; activin or inhibin-related activities; chemotactic or chemothactic activities; broliferation or metastrasis.

CC chemotactic or chemothactic activities; polypeptides and nuclectides of involved in noncognesis, cancer cell proliferation or metastrasis.

CC thrombolytic activities; receptor or ligand activities; or may be not be not their biological activities, polypeptides and nuclectides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions and cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell sophemial sohaemia, bone disorders (e.g., wiselooperosis), and abnormal configerative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., wiselooperosis), and conditions are cell for nucleic acids encoding them) may be used to promote cell growth. For example, such polypeptides may be used to promote cell growth. For e Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; haematopolesis chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphold cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascutopic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject Claim 1; Page 805; 1963pp; English. RI; 05-FEB-2001; 2001WO-US03800. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875. Drmanac e.g. arthritis and cancer WPI; 2001-457740/49. P-PSDB; ABB11916. (HYSE-) HYSEQ INC Tang YT, Liu C, WO200157188-A2 Homo sapiens. 09-AUG-2001

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258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; repliratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening;
may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
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319 AACTGGATTCGCAACATTGAGGAGGACGTCTGCAGACGTCGAAAAGATGATATCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
                                                                                                                                                                                                                        IleTrpAspThrAlaGlyGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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                                                                                                                                                                                                                                                                                  LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerH1sIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                        Sequence 1986 BP; 519 A; 545 C; 469 G; 453 T; 0 other;
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                                                                                                                             Conservative:
Mismatches:
                                                                                                   Length:
Matches:
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545.00
77.01%
52.94%
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                                                                                                                                                       49.328
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                                                                                                                             Percent Similarity:
                                                                                     Aliqnment Scores:
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polyunclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens and the use of ovarian antigens and the use of ovarian antigens and polynuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian covary and/or breast-related disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian or breast origin, reproductive system (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dymenorrhoes), endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and unmunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), crespiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polymorlectides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymorlectides may be used as ford additives or to prepare antibodies cuseful in disease diagnosis, drug targeting and phenotyphing. The present sequence or prepares or the present conting a human ovarian antigen of the
                          neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; ne antiinflammatory; gynaecological; reproductive; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 290; 2922pp; English.
                                                                                                                                                                                                                                                                                                SCI INC
                                                                                                                                                                                                                                                     07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological diseases
                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABP41333
                                                                                                                           WO200200677-A1.
                                                                                      Homo sapiens
                                                                                                                                                                    03-JAN-2002
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.

Sequence 2411 BP; 600 A; 671 C; 583 G; 547 T; 10 other;

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2411
98
45
43
                         Conservative:
Mismatches:
Indels:
        Length:
Matches:
                                                     Gaps:
        2.28e-52
540.00
76.88%
52.69%
48.87%
                         Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                          Query Match
                   Score:
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2 AlaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGlyLys 21 US-09-817-198B-2 (1-212) x ABQ54410 (1-2411)

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406
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                                                                                                                                                                                                                                                                                                                                                                                                        467 GACTATGGAATCAAGTTCATGGAGACCAGCGCGAAGGCCAACATCAATGTGGAAAATGCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; synecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease; ds.
47 GCGAAGACCTACGATTACCTGTTCAAGCTGCTGCTGATCGGGGACTCGGGGGTGGGGAAG 106
                                                                                                     82 GlnGlyllePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                     162 PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg 181
                                                                                      61
                                                                                                                                            62 TrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAla 81
                                                                                                                                                                                                                       42 GlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIle
                                                                                                                                                                                                                                                              102 TrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsn
                                                                                                                                                                                                                                                                                         347 IGGATICGCAACATIGAGGAGCACGCCTCTGCAGACGTCGAAAAGATGATACTCGGGAAC
                                                                                                                                                                                                                                                                                                                                                                             142 GluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer
                           22 ThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer associated gene sequences, referred to as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung cancer associated polynucleotide sequence SEQ ID 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF18072 standard; DNA; 1274 BP
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P-PSDB; AAB58196.
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GGCAACAAGCCTCCCAGTACȚGACCTGAAAACTTGTGACAAGAAGAA-CACCAACAAGTG 730

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731 CTCCCTGGGCTGAGGACCCTTTCTTGCCTCCCCACCCCGGAAGCTGAACCTGAGGGAGAC 790

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LeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGlu

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                                                                                                                                                                                                                           numerous other
                                                                                                                                                                                                                     chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, and proliferative gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences ARF18425. AAF18433 and peptide AAB5849 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                         associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treatment, prevention, and diagnosis of disorders
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GCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGGAAAC
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                                                                            sequences AAF17982 - AAF18424 encode human lung cancer
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1274 BP; 416 A; 267 C; 353 G; 235 T; 3 other;
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102
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Matches:
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Indels:
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                                              Claim 1; Page 566; 1425pp; English
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48.37%
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Best Local Similarity:
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such as lu
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This invention describes a novel human Rablo cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes the human Rablo protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer 39
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197 GluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrp
                        791 AACGCCAGAGGGAGTGAGCAGGGGGAGAATAGCAGAGGGGCTTGG
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                                                                                                                                                                          Human; Rabl0; Yap/Rab family; ss.
                                                                          BP.
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                                                                         AAA40104 standard; cDNA; 716
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Best Local Similarity:
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                                                              395 AGCAAATGGCTTAGAACATAGATGAGCATGCCAATGAAGATGTGGAAAGAATGTTACTA
                                               MetAlaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal
                                                                                                                                                ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
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     Gaps:
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                                                                                                                                                                                                                                  coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rabio. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes thuman Rabio protein described in the method of the invention.
198 ACCATAGGAATAGACTTCAAGATCAAAACAGTTGAATTACAAGGAAAGAAGATCAAGCTA 257
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                        60 GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
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coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes a canine Rablo protein described in the method of the invention.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a mammalian RAB protein. RAB proteins constitute the largest family of small GTPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of the gene in a biological specimen.
                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 GGAAACAAGTGTGATATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAGAACAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 GGGAAGACCTGCGTCCTTTTTCGGATGATGCCTTCAATACTACCTTTATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 ThrileGlyValAspPheLySMetLySThrIleGluValAspGlyIleLySValArgile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
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                                                                                                                                    Buckler
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 38-39; 58pp; English.
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                                                                                                                                  Abel K, McIntosh B,
13-MAR-2000; 2000WO-US06330
                                            99US-0126083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530.50
82.56%
55.81%
48.01%
                                                                                        (AXYS-) AXYS PHARM INC
                                                                                                                                                                            2000-647233/62.
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Best Local Similarity:
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                                            25-MAR-1999;
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EP1074617-A2.
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                                                                                                                                                                                                                                                                                                     neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, granecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat glassification, as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                  140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                                                                                                                                                                                                                                                                        Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
                                                                                                                                                                                                                                                        prostate cancer antigen nucleotide sequence SEQ ID NO:631.
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                                                             160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171
                                                                                           607 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 642
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                                                                                                                                                           BP
                                                                                                                                                          AAF16196 standard; cDNA; 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                         13-MAR-2001 (first entry)
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                                                                                                                          RESULT 12
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Length:
Matches:
Conservative:
Mismatches:

1.56e-51 530.50 82.56% 55.81%

> Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Indels:

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832
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                                    100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                                                                                                                               120 GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                   140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                            40 ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgIle
                                                                                                                                                                                                                                                     1 MetalaLysGln---TyrAspValLeuPheArgLeuLeuLeuIeGlyAspSerGlyVal
                                                                                                                                                                                 60 GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                                                                                                                                                                                       80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
                                                                         20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1013 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171
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, Sugiyama T, Wakamatsu A, Nagai K,
US-09-817-198B-2 (1-212) x AAF16196 (1-1537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH17889 standard; cDNA; 3533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
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160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171

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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length coDNAs defined in the specification, and for the detection PT full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

X X X Claim 8; SEQ ID 17618; 2537pp + CD ROW; English.

XX C The present invention describes primer sets for synthesising 5602 cc cmprises: (a) an oligo-dr primer sets for synthesising 5602 cc cmprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprisising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the oligonucleotide comprises a 1'-end sequence complementary to the oligonucleotide comprises a 3'-end sequence complementary to the oligonucleotide comprises a 1'-end sequence complementary to the specification. The primer sets can be used in antisense therapy and the specification. The primers are useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AMH3333 represent human amino acid sequences; and AMH3639 to AMH3832 cc represent oligonucleotides, all of which are used in the exemplification of coff the present invention.

XX Sequence 3533 BP; 967 A; 716 C; 730 G; 1120 T; 0 other;
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SQ Sequence 3533 BP; 967 A; 716 C; 730 G; 1120 T; 0 other;
Alignment Scores:
4.85e-51 Length: 3533
Score: 530.50 Matches: 96
Percent Similarity: 82.56% Conservative: 46
Best Local Similarity: 55.81% Mismatches: 29
Best Local Similarity: 22 Gaps: 1

US-09-817-198B-2 (1-212) x AAH17889 (1-3533)

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.00 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                                                  GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
                                                                                                                                                                                                                                                                                                              140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                                                                                                                                                                                                                                                                                                          ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgIle 59
                                                                                                                                 GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg 79
                                                                                                                                                                            80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnH1sIle 99
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                                                                                                                                                                                                                                                                                GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
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The invention relates to isolate to purpute (1) and to polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and call against coding sequences. AASA4197-AASA4564 represent novel human classed acquence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 674 BP; 218 A; 136 C; 173 G; 147 T; 0 other;
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96
46
29
980 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 1015
                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #7257.
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Mismatches:
Indels:
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                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                          AAS71453 standard; cDNA; 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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82.56%
55.81%
47.92%
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG07266.
                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital anomaly; pulmonary congestion; oedema; heemorrhage; adult respiratory distress syndrome; Goodpasture's syndrome; chronic obstructive pulmonary disease; asthma; pulmonary hypertension; liver disorder; hepatic injury; jaundice; cholestasis; viral hepatitis; cirrhosis; Wilson's disease; autoimmune hepatitis; hepatic failure; brain disorder; hypoxia; cerebral isochemia; intracranial haemorrhage; acute meningitis; Parkinson's disease; Alzheimer's disease; glioma; chronic bacterial meningoencephalitis; multiple sclerosis;
                                       20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                40 ThrileGlyValAspPheLySMetLysThrileGluValAspGlyIleLysValArgile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein; 32705; 23224; 27423; 32700; 32712; lung disorder;
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                                                                                                                                                                                                                                                                                                                                                                                           555 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 590
                                                                                                                                                                                                                                                                                                                                                                              160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of human 27423 G-protein.
Gaps:
                 US-09-817-198B-2 (1-212) x AAS71453 (1-674)
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18..641
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The present sequence encodes a human G-protein. The specification describes 32705, 23224, 27423, 32700 or 32712 small G-proteins The G-protein polypeptides and polynucleotides are useful as a target for diagnosis and treatment of G-protein mediated or related disorders, and for identifying agonists and antagonists for diagnosis and treatment. They are useful for treating disorders of lung (e.g. congenital anomalies, pulmonary congestion, oedema, adult respiratory distress syndrome, haemorrhage, chronic obstructive pulmonary disease, asthma, Goodpasture's syndrome and pulmonary hypertension, liver (e.g. hepatic injury, jaundice, cholestasis, viral hepatitis, cirrhosis, Wilson's disease, autoimmune hepatitis and hepatic failure), and correcting meningeneral ischemia, intraoranial haemorrhage, chronic conditions and pulmonary disease, gliomas, chronic charterial meningeneral schemial, intraoranial haemorrhage, corte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377
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brain disorders
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                 Novel human small G-protein polypeptides and treating lung disorders, liver disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis, stroke and Huntington's disease).
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                                                                                                                                                                                                                                                                                                     Claim 2; Fig 15; 151pp; English.
                                                  (MILL-) MILLENNIUM PHARM INC
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528.50
80.68%
53.98%
47.83%
29-FEB-2000; 2000US-0185606
                                                                                                                                                      WPI; 2001-550182/61.
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                                                                                                                                                                              P-PSDB; AAG67154
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438 ATTGACTATGGGATTAAATTCTTGGAGACAAGCGCAAAATCCAGTGCAAATGTAGAAGAG 497

qq

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Search completed: June 23, 2003, 11:10:07 Job time: 232 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2003, 10:52:29; Search time 1383 Seconds

(without alignments)
2482.605 Million cell updates/sec

105-09-817-198B-2

Perfect score: 105
Sequence: 105
Sequence: 105
Sequence: NARQYDVLFRLLLIGDSGVG......LEEEEGKFEGFANSSKTCWC 212

Scoring table: BLOSUMG. Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 7.0
Pelop 6.0, Pelext 7.0
Pelop 6.0, Delext 7.0
Pelop 6.0, Delext 7.0
Minimum DB seq length: 0
Maximum Match 08
Maximum Match 08

Post-processing: Minimum Match 08
Listing first 45 summaries
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COMMAND Line parameters:
-WODEL-frame+_p2n.model -DEV-xlh
-Q-Cogn2_L/USPTQ_spool/USOS911198/runat_18062003_144633_27919/app_query.fasta_1.391
-Q-Cogn2_L/USPTQ_spool/USOS911198/runat_18062003_144633_27919/app_query.fasta_1.391
-DB-EST -QFW-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-bloam62 -TRANS-bluman40.cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LCCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-20000000
-USER-USOS917198_cCGN_1_1_1906_cUnnat_18062003_144633_27919 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THRRADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FCAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

em_gss_other:* em_gss_pro:* em_gss_rod:* ew_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_gss_fun:* em_gss_mam:* #:enw_es6_me em_estfun: em_estom:* em_estro:* em_htc:* gb_estl:* em_esthum: em_estmu:*
em_estov:*
em_estpl:* em_estba:* gb_est3:*
gb_est4:*
gb_est5:* em_estin: db_gss:* gb_est2 EST:* Database :

RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID 956 90.1 1091 12 BF160330 958.5 86.3 932 12 BF156424 914 82.7 992 12 BF167888 918 82.7 992 12 BF167888 918 82.7 992 12 BF178163 918 82.7 992 12 BF178163 918 82.7 992 12 BF178163 919 90.1 1091 12 BF178163 910 82.4 616 13 BF1781633 911 82.7 992 12 BF178163 918 92.7 992 12 BF178164 919 92 12 BF178163 910 92 12 BF178163 910 93 12 BF178163 911 94 82.7 992 12 BF178164 912 92 12 BF178164 913 92 12 BF178164 914 82.7 992 12 BF178165 916 93 12 BF178165 917 70.3 814 12 BF178165 918 92 12 BF178165 919 92 12 BF178165 910 92 12 BF178165 910 93 11 13 BF168201 911 13 BF168201 912 93 11 13 BF168509 913 12 BF178165 914 82.7 992 12 BF178165 915 62.8 485 12 BF168101 918 92.3 10 BF178165 918 92 12 BF178165 919 92 12 BF178165 910 91 13 BF178165 910 91 91 13 BF178165 910 91 91 13 BF178165 910 91 91 91 91 91 91 91 91 91 91 91 91 91	Score Match Length DB ID Description 953.5 80.1 101 12 BF535642 BF160330 BF160330 BF160330 BF160330 BF160330 BF160330 BF160330 BF160530	Score Match Length DB ID Description 953.5 60.1 1091 12 BF160330 BF156430 BF156430 BF156430 BF156430 BF156430 BF156430 BF156430 BF164858 BF164854 GG BF164854 GG BF164854 GG BF164854 GG BF164857 GG BF164854 GG BF164854 GG BF164854 GG BF164854 GG BF164854 GG BF164854 GG BF18165 GG BF181665 BF181665 GG BF181665 GG GG <th>Score Match Length DB ID Description 953.5 86.3 92.1 12.875542 BF535642 BF535642 953.5 86.3 93.2 12.8173542 BF535642 BF535642 BF535642 92.6 83.4 616 13.81564888 BF107130 BF535642 BF535622 BF535933 BF535933 BF535933 BF535933 BF535933 BF535933 BF535933 BF53622 BF53622 BF53622 BF53934 BF539344 BF53934 BF53934 BF53934</th> <th></th> <th></th> <th>øР</th> <th></th> <th></th> <th>SUMMARIES</th> <th></th>	Score Match Length DB ID Description 953.5 86.3 92.1 12.875542 BF535642 BF535642 953.5 86.3 93.2 12.8173542 BF535642 BF535642 BF535642 92.6 83.4 616 13.81564888 BF107130 BF535642 BF535622 BF535933 BF535933 BF535933 BF535933 BF535933 BF535933 BF535933 BF53622 BF53622 BF53622 BF53934 BF539344 BF53934 BF53934 BF53934			øР			SUMMARIES	
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	30 1091 bp mRNA linear EST 30-OCT-2000	601768601F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987745 5',	equence.	. 08	BF160330.1 GI:11040541		mouse.	sculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 1091)	NIH-MGC http://mgc.nci.nih.gov/.	National Institutes of Health, Mammalian Gene Collection (MGC)	
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BF160330	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

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AUTHORS
TITLE
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                                                                                                                                                                                          1. .1091
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                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can if cound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9195 row: b column: 02
High quality sequence stop: 654.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (Bases I to 932)
INIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jéffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LINL)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9525 row: m column: 09
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Location/Qualifiers
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                                                                                                                                                                                                                                                                               BF535642 93.2 bp mRNA linear EST 11-DEC-2000 602054039F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193456 5',
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euArgMetArgAlaSer-AsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLys
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. CE 1 (bases 1 to 616)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Dubublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Cgapbs-rémail.ih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

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High quality sequence start: 2

High quality sequence stop: 614.
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AUTHORS
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JOURNAL
COMMENT
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BI648588
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992 bp mRNA linear EST 19-OCT-2000 601753464F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3981183 5', mRNA sequence.
BF101730
BF101730.1 GI:10884256
EST.
Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (199)." Il54 c 179 g 115 t 1 others
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                   47
                                                                                                                                                                                    84
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                                                                                                                                                                                                                                               87
                                                                                                                                                                LysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyrGlyMetAspPhe
                                                                           616
180
3
1
1
                                                                                            Conservative:
Mismatches:
Indels:
                                                                           Length:
Matches:
                                                                                                                             Gaps:
                                                                                                                                               (1-616)
                                                                                                                                               US-09-817-198B-2 (1-212) x BI648588
                                                                           8.89e-108
922.00
98.92%
97.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                               Percent Similarity:
Best Local Similarity:
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                                     167
                                                                  Alignment Scores:
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DB:
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AUTHORS
TITLE
JOURNAL
                                     BASE COUNT
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BF178163.1 GI:11056305
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910.00
97.28%
96.20%
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BF178163
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                                                                                                                                                                                                                                                                         /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"

272 c 306 g 163 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AAGACATGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9177 row: p column: 16
High quality sequence stop: 706.
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                                                                                                                                                    1. :992
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
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Mismatches:
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Matches:
Contact: Robert Strausberg, Ph.D.
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Musucatura Butteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 902)

In 1 (bases 1 to 902)

In Mil-MCC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys contact: Mobil Library Preparation: Life Technologies, Inc.

Clona Library Preparation: Life Technologies, Inc.

Clona Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM320 row: f column: 22

High quality sequence stop: 603.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                            BF178163 ' 902 bp mRNA linear EST 31-OCT-2000 601809083F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4039701 5',
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                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; S1te_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .902
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/lab_host="DH10B"
                                                                                                             Conservative:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 699)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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BI557933
EBI557933.1 GI:15445247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 TACCAGACTATCACAAAGCAGTACTATCGGCGAGCCCAGGGAATATTTTAGTCTACGAC
                                                                          IleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGluTyr
                                                                                                                                                                                                                                       GlnValGlyArgGluGlnGlyGlnGlnLeuAlaLys-GluTyrGlyMetAspPheTyrGl
                                                                                                                                                                                                                                                                          314 CAGGIGGGGAGAGAGCAGGGCAGCAGCIGGCIAACGGAGIACGGCAIGGACTICIACGA
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BIS57933
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BF966292 796 bp mRNA linear EST 23-JAN-2001 602286692F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375366 5', mRNA sequence.
BF966292.1 GI:123333507
    Nature Genetics
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
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    et
Reference for transgenic model: Xu 22, 37-43 (1999)."
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Mismatches:
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BF181167 1100 bp mRNA 11near EST 31-OCT-2000 601805830F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036759 5',
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                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1100)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contract: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM9312 row: 1 column: 08
High quality sequence stop: 606.
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BF181167.1 GI:11059309
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 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov h column: 23
High quality sequence stop: 663.
Location/Qualifiers
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/clone="IRAGE:4375366"
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Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E (1 (bases 1 to 616)

I (context: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CON Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM1034 row: f column: 06

High quality sequence stop: 616.

Location/Qualifiers
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BG247902.1 GI:12757717
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Site_2: NotI, cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM9312 row; h column: 09
High quality sequence stop: 712.
                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 others
                                                                                                                                                                                                                                                  1. .1121
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/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
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DB:
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                                         TITLE
JOURNAL
COMMENT
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             REFERENCE
AUTHORS
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/db_xref="taxon:9606"
/db_xref="Taxon:9606"
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ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGAGG(G). Size-selected >SOODp for average insert size
into EcoRI/XhoI sites using the following 5' adaptor:
GGGAGG(G). Size-selected >SOODp for average insert size
into EcoRI/XhoI sites using the following 5' adaptor:
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into EcoRI/XhoI sites using the following 5' adaptor:
GGAAGG(G). Size-selected >SOODp for average insert size
into EcoRI/XhoI sites using the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |#
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BG762967.1 GI:14073620 .
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160 luSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArg---LysGluLeuGluG
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602844184F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979781 5',
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NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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                                    GluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuVal
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information or life through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0978 row. h column: 22
High quality sequence stop: 647.
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; S1te_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation? 7:311 (1996)."
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603278051F1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5318388 5',
mRNA sequence.
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NIH-WGC http://mgc.nci.nh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nh.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Best Local Similarity:
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                                                                                                                                                             Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998
                                                                                                                                                                                                                                              Query Match:
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Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="INAGE:366417"
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/tab_nost="nenths"
/note="corpan: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 ATTTGGGACACAGCAGGCAGGAGAGGTACCAGACTATCACAAAGCAGTACTATCGGCGA 396
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I to 618)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   uy86b05.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666417 5' similar to SW:RB15_RAT P35289 RAS-RELATED PROTEIN RAB-15. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLySGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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High quality sequence stop: 4
Location/Qualifiers
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BFI50465.1 GI:11031860
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     DEFINITION
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KEYWORDS
SOURCE
                                                                                                                            ORGANISM
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COMMENT
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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
22, 37-43 (1999)."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov blate: LLAM1807 row: e column: 13 High quality sequence stop: 777. Location/Qualifiers
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112 GluGlyValGlnLysIleLeuIleGlyAsnLysAlaAspGluGluGlnLysArgGlnVal
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I (bases I to 1767)

S NIH-MGC http://mgc.nci.nih.gov/.

INTH-MGC http://mgc.nci.nih.gov/.

Interpolation Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence start: 89

High quality sequence stop: 574.

Location/Qualifiers

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                                                                                                                                                                                                                                    AGENCOURT_6424626 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491242
5', mRNA sequence.
BM462147.1 GI:18511187
EST.
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                                            121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                       517 AATAATGCTGATGAAGAGCAGAAACCGCAGGTGGGGAGAGAGCAGGTGCAGCAGCTGGC 576
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AUTHORS
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APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-865-4166
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US-09-454-818-3
US-09-415-522-1
US-09-233-170-6
US-09-387-341-1
US-09-325-932A-29
US-09-325-932A-29
US-08-306-6918-16
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US-08-89-738-1
US-08-771-212A-1
US-08-842-3066-48
US-08-88-9738-48
US-09-078-317-1
US-09-454-818-1
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US-08-306-691B-15
PCT-US93-06251-29
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US-08-741-411-6
US-08-247-946A-5
PCT-US95-06420-5
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals
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Patent No. 5892012
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Command line parameters:
-WODEL-frame+_p2n.model.-bEV-xlh
-Q-/cgn2_1/USPTO_spool/US09817198/runat_18062003_144633_27928/app_query.fasta_1.391
-Q-/cgn2_1/USPTO_spool/US09817198/runat_18062003_144633_27928/app_query.fasta_1.391
-Q-/cgn2_1/USPTO_spool/US09817198_fasta_p.sur_x-p2n.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START-1 -END--1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_AMX=100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09817198_gcGTN_11.40_frunat_18062003_144633_27928 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARR_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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1547.987 Million cell updates/sec
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1105
1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                      GenCore version 5:1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                             OM protein - nucleic search, using frame_plus_p2n model
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US-09-154-602-4
US-08-824-873-2
US-09-075-454-10
US-09-075-454-10
US-09-399-913-66
US-08-773-423-4
US-08-773-423-4
US-08-773-423-4
US-09-795-454-13
US-09-493-914-1
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
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Score

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Database :

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Searched:

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Sequence:

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 CAGTGGCTGCAGGAGATTGACCGCTATGCCAGCGAGAACGTCAATAAGCTCCTGGTGGGC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 AACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCCACGAGGAGTTTGCA 485
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Mismatches:
Indels:
                                                                                                                                                                                                                                                              US-09-817-198B-2 (1-212) x US-08-916-901-4 (1-925)
                                                                                                                                                                 Length:
Matches:
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Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: COTIEY, Neil C.
        SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRTUT04
CLONE: 2514506
US-08-916-901-4
                                                                                                                                                                           478.50
65.84%
45.05%
43.30%
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-154-602-4
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246 ATCTGGGACACAGGGGCCAGGAACGGTTCCGGACCATCACTTCCAGCTACTACCGGGGG 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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Conservative:
Mismatches:
Indels:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-817-198B-2 (1-212) x US-09-154-602-4 (1-925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHRARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478.50
65.84%
45.05%
43.30%
                                                                                                                                                                      COMPUTER READABLE FORM MEDIUM TYPE: Disket
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CLONE: 2514506
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                     94304
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Pred. No.:
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                             426 AACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCACAGGCCAAGGAGTTTGCA 485
                                                                                   486 GACTCTCTGGGCATCCCCTTCTTGGAGAGGGGCCCAAGAATGCCACCAATGTCGAGCAG 545
                                                                                                                         161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                     591 GGAGCAGCCTCTGGGGGGGGGGGCCCAATCTCAAGATCGACAGCACCCCTGTAAAGCCG 650
AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                              141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                      546 GCGTTC------ATGACCATGCTGCTGCTGAAATCAAAAGCGGATGGGGCCT 590
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/824,873
FILLING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegier, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0240 US
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FILING DATE:
NAME: BILLINGS, Lucy J.
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
"wor: nucleic acid
                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08824873
Patent No. 5843717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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67.84%
45.23%
39.59%
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MEDIUM TYPE: Diskette
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IMMEDIATE SOURCE:
LIBRARY: PANCNOTO4
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Best Local Similarity:
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Pred. No.:
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DB:
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                                                                                                                                                                                                                                                                                     83
                                                                                                                      25 Leu-CysArgPheThrAspAsnGluPhe---HisSerSerHisIleSerThrIleGlyVa 43
                                                               22 TACGACGTCGCCTTCAAGGTCATGCTGGTGGGGGACATCGGGTGTGGGGAAGACCTGTCT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 yllePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLysTrpVa
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                                          TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCysLeu
                                                                                                                                                                                                        lAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAs
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; Sequence 2, Application US/09198184
; Patent No. 6010859
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
: TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fast-SEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUTCATION INFORMATION:
TELEFHONE: 650-895-0555
TELEFAX: 650-845-4166
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,454
FILING DATE: Herewith
CLASSIFICATION:
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     APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
APPLICANT: Batra, Sajeev
APPLICANT: Batra, Mariah R.
TITLE OF INVENTION: MAS PROTEINS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.13e-45
429.00
68.48%
44.57%
38.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: UCMCL5T01
CLONE: 1528559
                                                                                                                                                                  STREET: 3174 PortITY: Palo Alto STATE: CA COUNTRY: US
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 rArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetAr 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 lAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PThralaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGl 83
                                                                                                                                                                                                                                                                                                                                                                                                                            25 Leu-CysArgPheThrAspAsnGluPhe---HisSerSerHisIleSerThrIleGlyVa 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 lSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 aAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTy
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                             US-09-817-198B-2 (1-212) x.US-09-198-184-2 (1-1340)
                                                                                                                                                                                                                                                                                 Length:
Matches:
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                    PF-0240 US
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Patent No. 6391580
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0;
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPRAX: 415-865-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCNOT04
CLONE: 738957
                                                                                                                                                                                                                                                                              6.5e-46
437.50
67.84%
45.23%
39.59%
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Best Local Similarity:
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US-09-075-454-10
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                                                                                                                                                                                                                                                                                 556 -----GAGTTAGCCTTTCTGGCCATCGCCAAGGAA------CTGAAATACCGG 597
                                                                                                                                                                                   144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
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                                                                                                                                     511 GGTGTTCCCTTCCTGGAGACCAGCCCAAGACTGGCATGAATGTG-------
                                                 SerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: An, Wenqian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070C9
CURRENT APPLICATION NUMBER: US/09/399,913
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85
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Conservative:
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Indels:
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EARLIER APPLICATION NUMBER: USSN 60/110,277

EARLIER FILING DATE: 1998-11-30

EARLIER FILING DATE: 1998-11-25

EARLIER FILING DATE: 1998-11-25

EARLIER FILING DATE: 1998-11-25

EARLIER FILING DATE: 1998-11-20

EARLIER APPLICATION NUMBER: USSN 60/109,333

EARLIER APPLICATION NUMBER: USSN 69/298,731

EARLIER APPLICATION NUMBER: USSN 69/298,731

EARLIER FILING DATE: 1999-04-23

EARLIER FILING DATE: 1999-07-09

EARLIER FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66, Application US/09399913
Patent No. 6361971
GENERAL INFORMATION:
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64.59%
40.67%
37.92%
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                                                                                                                                                                                                                                                                                                                                                  598 GCCGGCCATCAG 609
                                                                                                                                                                                                                                                                                                                  184 AlaSerAsnGlu 187
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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US-09-399-913-66
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-399-913-66
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LENGTH: 639
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                                                                                                                                                                              GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 IlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLysTrpVal 103
                                                                    ACTGAGATTCATGACTATGCCCAGAGGGACGTGGTGATCATGCTGCTAGGCAACAAGGCG 431
                                                                                                                                   164 ArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg 183
                                                                                                                                                                                                                                                                                -----GAGTTAGCCTTTCTGGCCATCGCCAAGGAA------CTGAAATACCGG 578
SerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAla 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThralaGlyGlnGluArgTyrGlnThrileThrLysGlnTyrTyrArgArgAlaGlnGly 83
                                                                                                                                                                                                   ||||::: ||| |||||||||||| ||| :::|||:::
|GTGTTCCCTTCCTGGAGACCAGGCTGGCATGAATGTG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuCysArgPheThrAspAsnGluPheHisSer---SerHisIleSerThrIleGlyVal
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US-09-484-970B-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-817-198B-2 (1-212) x US-09-484-970B-142 (1-2612)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 142, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: JOHES, KATEN A.
APPLICANT: WAINEL, MICHAELI GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEC ID NOS: 172
LENTH: 2612
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429.00
68.48%
44.57%
38.82%
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                                                                                                                                                                                                                                                                                                                184 AlaSerAsnGlu 187
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                US-09-484-970B-142
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312 GCCITATIGGITIATGACATIGCTAAACAICTCACATAIGAAAAIGIAGAGGGAIGGCG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyr 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPhe--- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 LeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyVal 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 ACAGCAGGCAAGAGCGATATCGAGCTATAACATCAGCATATTATCGTGGAGCTGTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AAAGAACTGAGAGATCATGCTGATAGTAACATTGTTATCATGCTTGTGGGCAATAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 GGTTTGTCATTCATTGAAACTTCGGCCCTAGACTCTACAAATGTAGAAGCTGCTTTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 ThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg---
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SCHERING 3.0-017 CIP CIP CIP
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85
868
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..970
OTHER INFORMATION: /note= "Y2H9"
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US-08-773-423-4
; Sequence 4, Application US/08773423
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 7.94e-43
411.50
64.04%
41.87%
37.24%
  REFERENCE/DOCKET NUMBER:
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672 AAGCCAAAG 680
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                                                                                                                                                                             TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                           US-08-888-077A-28
                                                                                                                                                                                                                                                                                                                     Alignment Scores
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                                                                                                                                                                                                                                                                                                                                                                                                                        MetaspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArg 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 LeuThrGluLeuVal-LeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg-- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AlaSerAsnGluLeuAlaLeuAlaGluLeu-----------GluGluGl 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGCTACACTITACAGACAAGAGGTITCAGCCGGTGCATGACCTCACAATTGGTGTAGAG 126
                                                                                                                                                                                                                                      85 PheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSer 104
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                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                   AspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAlaAsp
                                                                                                                                                                                   ACAGCAAAAGAAATTTATGAAAAATCCAAGAAGGGGTCTTTGACATTAATAATGAGGCA
    LeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyValAsp
                                                                                PheLysMetLysThr11eGluValAspGlyIleLysValArgIleGlnIleTrpAspThr
                                                                                                                                                            65 AlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIle
                                                                                                                                                                                                                                                                                                                                                                                               125 GluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 CITAICITCAIGGAAACITCIGCCAAGACITCTAAIGIAGAGGAGGCAITIAITAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASEN, JOHNNA M
APPLICANT: FRASEN, PAULE
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
PILING DATE: 03-JUL-1997
CLASSTRICATION 530
PRIOR APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uGluGlyLysProGluGlyProAla 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 GGAGGCCAGCAGGCAGGGGAGGCT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,629
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123 AlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGlu 142
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329 GGGGCCCTCCTGGTGTTGACCTAACCAAGCACCAGACCTATGCTGTGGTGGAGCGATGG 388
                                                                                                                                                        449 AGTGACCTCAGCCAGGCCGGGAAGTGCCCACTGAGGAGGCCCGGAATGTTCGCTGAAAAC 508
                                                                                                                                                                                                                                                                                                                                                         182 MetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGlu 201
                                                                                                                                                                                                                                                                                                                                                                                                --- AGTGCCCAGGNTGGACAGGAGCCT 673
                                                              569 GAGACTGTCCTGAAAGAAATCTTTGCGAAGGTGTCCAAGCAGAGAGAAGAACAGCATCCGG
                                       103 ValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLys
                                                                                                                                                                                                  143 TyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08741411
Patent No. 6124116
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                              629 -----ACCAATGCCATCACTCTGGGC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                       202 GlyProAlaAsnSerSerLysThrCys 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            674 GGCCCTGGGGAGAGAGGGCCTGTTGC 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,411
FILING DATE: Herewith
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ATTORNEY/AGENT:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 890 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abba.
STREET: 31/-
TTY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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STATE: CA
COUNTRY:
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US-08-741-411-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 GAAGATTATAAACTTTGTCTTCAAGGTGGTGCTGATCGGCGAATCAGGTGGGGAAGAC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValaspPheLysMetLysThrIleGluValaspGlyIleLysValargIleGlnIleTrp 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LysGlnTyrAspValLeuPheArgLeuLeuLeulleGlyAspSerGlyValGlyLysThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGly 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 GITGAGTICICCACCCGCACTGIGAIGTIGGGCACCGCTGCTGAAGGCTCAGAICTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                        CURRULES.

CORRULES.

CORRUPTION SYSTEM:

SOFTWARE: FastSED for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/773,423

FILING DATE: Herewith
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                        APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0183 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: B1111ngs, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373.00
59.818
36.848
33.768
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LENGTH: 847 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus
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Best Local Similarity:
Query Match:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                               COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrGlyMet---AspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 MetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGlu 201
                                                                                                                                                                                                                                             132 TACGTCCACCAGCTCTTCTCCCAGCACTACCGGGCCACCATCGGGGTGGACTTCGCCCTC 191
                                                                                                                                                                                                                                                                                           ValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                  432 TGTGACCAGAACAAGGACAGTAGCCAGAGTCCTTCCCAGGTGGACCAATTCTGCAAAGAA 491
                                                                                                                                                                    72 CTGTACAAGTTGCTGGTGATTGGCGACCTGGGCGTGGGSAAGACCAGYATCATCAACAGC 131
                                                                                                                                                                                                                47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 CCTAATGAAGAAAACGATGTGGACAAAATTAAGCTAGATCAAGAGACCTTGAGAGCAGAG
                                                                                                                                                                                                               28 PheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyValAspPheLySMet ::: ::: ::: ::: ::: ::: :::
                                                                                                                                                     LeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCysLeuLeuCysArg
                                                                                                                                                                                                                                                                           LysThrIleGluValAspGly---IleLysValArgIleGlnIleTrpAspThrAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCGGTTCCTAGTGGAGAAGATTCTTGTAAACCACCAAAGC-----
            890
76
45
74
14
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                                            Conservative:
Mismatches:
                                                                                                                     US-09-817-198B-2 (1-212) x US-08-741-411-4 (1-890)
              Length:
Matches:
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                                                                          Indels:
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APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Gordey, Nell C.
APPLICANT: Patterson, Chandra
APPLICANT: Batra, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09075454
Patent No. 6391580
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                 3.35e-34
                              343.00
57.89%
36.36%
31.04%
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                                      Percent Similarity:
Best Local Similarity:
Query Match:
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STREET: 3
Alignment Scores:
Pred. No.:
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                                 Score:
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306 TGATGTTACATGTGAGAAAAGCTTTCTTAACATACGAGAATGGGTAGATATGATTGAGGA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 TGCAGCCCATGAGACTGTTCCCATTATGCTGGTAGGAAACAAGGCTGACATTCGTGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 sThrileGluValAspGlyIleLysValArgileGlnIleTrpAspThrAlaGlyGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 rAspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 uArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuValTy
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                   NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUTCATION INFORMATION:
TELECHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                    SOFTWARE: Word Perfect 6.1/MS-DOS CURRENT APPLICATION NUMBER: US/09/075 AFA
                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.97e-34
340.50
60.31%
38.66%
30.81%
                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                        FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                      ZIP: 94304
OMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE:
; LIBRARY: OVARTUT10
; CLONE: 2703745
US-09-075-454-13
                                                                                                             COMPUTER: IBM CON OPERATING SYSTEM:
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Best Local Similarity:
Query Match:
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                                                    94304
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Pred. No.:
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CITY: Pa
STATE: CA
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123	432	486 159	DD 546 GATGAAGCCTCCAGATGCCTGGTG QY 179 GlyLeuArgMetArgAlaSerAsn ::: Db 582GGAAAT	Qy 198 GlyLysPro	Qy 207 rLysThrCysTrpCys 212 ::: Db 684 TAGGCACCTTTGCTGTGT 702	RESULT 13 US-09-075-454-8 Sequence 8, Application US/09075454 Patent No. 6391580	APPLICANT: Hillman, Jennifer L. APPLICANT: Tang, Y. Tom APPLICANT: Lal, Preeti	APPLICANT: Guegler, Karl J. APPLICANT: Corley, Nell C. APPLICANT: Patterson, Chandra APPLICANT: Batra, Sajeev APPLICANT: Baughn, Mariah R. TITLE OF INVENTION: RAS PROTEINS	COUNTRY: US COUNTRY: US COUNTRY: US COUNTRY: US CIP: 94304	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTED: TOP COMPUTED	COMPOTER: LEM COMPACTORE COMPOTER: MAN COMPACTORE CORRENT APPLICATION DATA: CURRENT APPLICATION DATA:	us/09/ th	APPLICATION NUMBER: 08/766,551 FILING DATE: DECEMBER 12, 1996 ATTORNEY/AGENT INFORMATION: NAME: CETTON MICHAEL C.	** REGISTRATION UNDER: 39,132 REFERENCE/DOCKET NUMBER: 9F-01 TELECOMMUNICATION INFORMATION: 650-855-0555	IELEEKA: 030-043-4100 ; INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:	. LENGTH: 11/2 DASE PAIRS ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear
Qy 142 uTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPh 162 	Oy 162 eThrargLeuThrGluLeuValLeuGlnalaHisArgLysGlu	Qy 177LeuGluGlyLeuArgMetArgAlaSerasnGluLeu 188 	RESULT 12 US-09-493-914-1 ; Sequence 1, Application US/09493914 ; Patent No. 6448073 . CENERAL TAPODARTION.	; APPLICANT: Uger, Dick ; APPLICANT: Uger, Elke		; TITLE OF INVENTION: Cancer Associated Antigen Encoding Nucleic Acid Molecules; TITLE OF INVENTION: and Uses Thereof; FILE REFERENCE: LID-5638; CURRENT APPLICATION NUMBER: US/09/493,914; CURRENT APPLICATION NUMBER: 05/09/493,914	V)	· ທ	Alignment Scores: 3.5e-31 Length: 1407 Pred. No.: 321.50 Matches: 83 Score: Farcent Similarity: 54.19% Conservative: 40 Best Local Similarity: 36.56% Mismatches: 66 Query Match: 29.10% Indels: 38 DB: 4 Gaps: 10	US-09-817-198B-2 (1-212) x US-09-493-914-1 (1-1407)	Qy 8 LeuPheArgLeuLeuLleGlyAspSerGlyValGlyLysThrCysLeuLeuCysArg 27	Oy 28 PheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyValAspPheLySMet 47 :::	Qy 48 LysThrlleGluValAspGlylleLysValArglleGlnIleTrpAspThrAlaGly 66	Qy 67 GlnGluargTyrGlnThrIleThrLysGlnTyrTyrargArgAlaGlnGlyIlePheLeu 86 :: 252 CAAGAAGATTTGGAAACATGACGAGGTCTATTACCGAGAAGCTATGGGTGCATTATT 311	Oy 87 ValtyraspileSerSerGluargSerTyrGlnHisileMetLysTrpValSerAspVal 106 :: ::: :::::	Qy 107 AspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLys 122

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nrGluLeuValLeuGlnAlaHisArgLysGluLeuGlu 178
::: ::|||
rGAAACACATACTT------581
                                                                                                                 nnGluLeualaLeualaGlu---LeuGluGluGluGlu 197
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\TGAGTGTGACCTAATGGAGTCTATTGAGCCGGACGTC 623
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                                                                                             1172
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Mismatches:
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                                                                                               Length:
Matches:
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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APPLICANT: Batra, Saleev
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09075454 Patent No. 6391580 GENERAL INFORMATION:
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Tang, Y. Tom
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Guegler, Karl J.
Corley, Neil C.
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Best Local Similarity:
IMMEDIATE SOURCE:
             LIBRARY: KIDNE CLONE: 627565
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90 IleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAsp----ValAspGlu 108
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                                                                                                                                                                                                                                                                                                                                                                    NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION INFORMATION:
TELEFRONE: 650-855-0555
TELEFRX: 650-845-4166
                                                                                                                                                                        SOFTWARE: Word Perfect 6.1/MS-DOS 6.2 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/075,454 FILING DATE: Herewith
                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1533 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATI
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Palo Alto
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Best Local Similarity:
Query Match:
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; CLONE: 1651593
US-09-075-454-11
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90 IleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAsp---ValAspGlu 108
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   522 AAGGTCATTGTGGGGGGGGCCTGTCGGTGGGGAAGACTTGCCTCATTAATAGGTTCTGC 581
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Job time : 46 secs
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                  147 PheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThr 166
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                                                                                                                                                             -----GTGCTGGCTGAGCTGGAAAATCGGGGGCTCGACGCATTGGG 1087
                                                                                                                                         187 GluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGly
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hallman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: GOI, SULVE HUMAN GTP-BINDING PROTEINS
NUMBER OF SEQUENCES: 9
NOMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALTA PORTER Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,551
                                                                                           1025 GCACTGACCTTTGAGGCCAAT---
                                                                                                                                                                                                                                                 Sequence 6, Application US/08766551
Patent No. 5840569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LIBRARY: SEQ ID NO:6
CLONE: 627051
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MEDIUM TYPE: Diskett
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Query Match:
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Sequence 885, App Sequence 886, App Sequence 836, App Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 646, App Sequence 13, App Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 66, Appli Sequence 68, Appli Sequence 188, Appli Sequence 188, Appli Sequence 188, Appli Sequence 189, Appli Sequence 159, Appli Sequence 159, Appli Sequence 159, Appli Sequence 159, Appli Sequence 189, Appli Sequence 653, Appli Sequence 563, Appli Sequence 159, Appli Sequence 159, Appli Sequence 159, Appli Sequence 653, Appli Sequence 159, Appli Sequence 653, Appli Sequence 159, Appli Appli Sequence 159, Appli Appli Sequence 159, Appli Appli Sequence 159, Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT332
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
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Patent No. US20020168711A1
GENERAL INFORMATION:
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                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-868-88
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Query Match:
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US-09-764-868-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
-WODEL-frame+_p2n,model -DEV=xlh
-Q=/Cgn2_1/GSPTO_spool/US09817198/runat_18062003_144634_27974/app_query.fasta_1.391
-Q=/Cgn2_1/GSPTO_spool/US09817198/runat_18052003_144634_27974/app_query.fasta_1.391
-LOOPCL=0 *LUDSPTO_spool/US09817198/runat_180FEXTX=blosum62
-TRANS=human40.cd1 *LIST=45 *DOCALIGN=200 *THR_SCORE=pct *THR_MAX=100
-THR_MNN=0 *ALIGN=15 *NODE=*LCAL *OUTFWT=pto *NORM=ext *HERPSTEZE=500 *MINLEN-0
-MAXLEN-200000000 *GSR=GSO9817198 *GCGN_1_1 57_crunat_18062003_144634_27974
-NCPU=6 *ICPU=3 *NO_MMAP *LARGEQUERY *NGS_SCORES=0 *WAIT *DSPBLOCK=100
-LONGLOG *DEV_TIMEOUT=120 *WARN_TIMEOUT=30 *THREADS=1 *XGAPOP=10 *XGAPEXT=0.5
-FGAPOP=6 *FGAPEXT=7 *YGAPOP=10 *YGAPEXT=0.5 *DELOP=6 *DELEXT=7
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Sequence 1, Appli
                                                                                                                                                            June 23, 2003, 11:10:12; Search time 158 Seconds (Without alignments) 1968.953 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                     OM protein – nucleic search, using frame_plus_p2n model
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US-09-764-868-507
US-09-925-302-91
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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length: 2000000000
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Score

Result ₽.

Total number of

Minimum DB seq Maximum DB seq

Title: Perfect score:

Run on:

Scoring table: Sequence:

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AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
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                                                                                                    IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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Fatent No. US20020168711A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PT32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILIG DATE: 2001.01-17
Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 507
LENGTH. 566
US-09-817-198B-2 (1-212) x US-09-817-198A-1 (1-3257)
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LOCATION: (493)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (538)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION:
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Patent No. US20020146758A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FestSEQ for Windows Version 4.0
SEQ ID NO 1
                                                LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
                                                                                                                                                                                                                                                                                                       MetAlaLysClnTyrAspValLeuPheArgLeuLeuLleClyAspSerGlyValGly
                             ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC
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Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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TYPE: DNA
ORGANISM: Human
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICANT: 000-108-10
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05918
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
LENGTH: 1274
                                                          266
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                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                      or
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                    n equals a,t,g,
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ORGANISM: Homo saplens
FEATURE:
NAME/KEY: misc feature
                                                                            Percent Similarity:
Best Local Similarity:
; NAME/KEY: SITE
; LOCATION: (563)
; OTHER INFORMATION:
US-09-764-868-507
                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                    192 AAGACTTGTCTGATCATTCGCTTTGCAGAGGACAACTTCAACAACATCTTCCACC
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                1274
102
54
55
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Matches:
Conservative:
Mismatches:
Indels:
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LOCATION: (1264)
OTHER INFORMATION: n equals a,t,g,
NAME,KEY: misc feature
LOCATION: (1268)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                           6.09e-59
534.50
66.38%
43.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 631, Application 6; Patent No. US20020151681A1; GENERAL INFORMATION:
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                  Alignment Scores:
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Percent Similarity:
Best Local Similarity:
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US-09-794-257-9

Sequence 9, Application US/09794257

Factor I No. US20020009804A1

GENERAL INFORMATION:

APPLICANT: MAYERS, Rachel

TITLE OF INVENTION: 92705, 23224, 27423, 32700, 32712, No. US20020009804A1e1

TITLE OF INVENTION: Human G-Proteins
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| ArgcGaagaaGaCGACGACGTTTTCAAGCTGCTCCTGATCGGGGATTCCGGAGTG 592
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Matches:
Conservative:
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Indels:
          CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 631
                                                                                                                                                                                                           LOCATION: (5)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                2.62e-58
530.50
82.56%
55.81%
48.01%
                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
FILE REFERENCE: PA101
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Best Local Similarity:
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Sequence 7, Application US/09794257

Sequence 7. Application US/09794257

Patent No. US20020009804A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1

TITLE OF INVENTION: Human G-Proteins
FILE REFERENCE: 35800/209286

CURRENT APPLICATION NUMBER: US/09/794,257

CURRENT FILING DATE: 2001-02-27

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 16
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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                                                                                                                                                                                                                                                                1.28e-58
528.50
80.68%
53.98%
                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: homo sapiens
US-09-794-257-9
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APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrey
APPLICANT: Bolt, Andrey
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOYEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
                                                                                                                                                                                                                                                                                                                                                                                     197
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498 GCATTTTTTACACTTGCACGAGATATAATGACAAAAACTCAACAGAAAA 545
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 879, Application US/09834975; Patent No. US20020110815A1; GENERAL INFORMATION:
                                                                                                                                       3.15e-58
528.50
80.68%
53.98%
47.83%
                                       TYPE: DNA
ORGANISM: homo sapiens
                                                                                      ; LOCATION: (18)...(641)
US-09-794-257-7
                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                  Percent Similarity:
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US-09-834-975-879
                                                                          NAME/KEY: CDS
                                                                                                                             Alignment Scores:
                         LENGTH: 1161
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Sequence 885, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
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Mismatches:
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Matches:
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: n - A,T,C
US-09-834-975-879
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                                                                                                                                                                                                                                          528.50
80.68%
53.98%
47.83%
                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                     NAME/KEY: misc_feature
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Best Local Similarity:
            SOFTWARE: Fasts
SEQ ID NO 879
LENGTH: 2497
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RESULT 11
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APPLICANT: Brown, Joffrey
APPLICANT: Born, Joffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-0169
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FASTSEQ for Windows Version
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OTHER INFORMATION: n = A,T,C or
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528.50
80.68%
53.98%
47.83%
                                                                                   ORGANISM: Homo sapiens
                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(2497)
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Best Local Similarity:
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
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Matches:
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CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 894
LENGTH: 2497
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Patent No. US20020110815A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C
US-09-834-975-894
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528.50
80.68%
53.98%
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP13(0) C USE CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR PELLING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-06-22 NUMBER OF SEQ ID NOS: 5379
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Mismatches:
Indels:
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Matches:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-836
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Matches:
Conservative:
Mismatches:
Indels:
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; TITLE OF INVENTION: OF HUMAN CANCERS
; FLEE REPERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 836, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
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528.50
80.68%
53.98%
47.83%
                                                                                                                                                                                                  ; LOCATION: (1)...(2497)
; OTHER INFORMATION: n - A,T,C
US-09-834-975-896
                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                       NAME/KEY: misc_feature
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Best Local Similarity:
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Sequence 48, Application US/10102806

Sequence 48, Application US/10102806

Publication No. US20030054421A1

GENERAL INFORMATION:

TILE CF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA103PLC1

CURRENT APPLICATION: NUMBER: US/10/102,806

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR PILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2001-08-10

PRIOR PILICATION NUMBER: PCT/US00/05881

PRIOR PILICATION NUMBER: 96/124,270

PRIOR PLICATION NUMBER: 60/124,270

PRIOR PLICATION NUMBER: 60/124,270

PRIOR PLICATION NUMBER: 60/124,270
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LOCATION: (937)
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SEQ ID NO 48
LENGTH: 939
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASLESO, for Windows Version 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-817-198B-2 (1-212) x US-09-967-736-4 (1-925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: B1111109S, LOLY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/967,736
FILING DATE: 28 Sep-2001
PRIOR APPLICATION DATA:

APPLICATION UNMBER: 09/154,602
FILING DATE: <a href="https://doi.org/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.1
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                                                                                                                              Lal, Preeti
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                              Sequence 4, Application US/09967736
Patent No. US20020103340Al
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Query Match:
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; ORGANISM: Arabidopsis thaliana US-09-770-445-529
                                       Alignment Scores:
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                        AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
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                                                              61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80
                                                                              APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
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Patent No. US2002023281A1
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
Davis, Keith R.
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                      Conservative: Mismatches:
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       Length:
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